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United States Department of Agriculture
Agricultural Research Service
National Program Staff
Beltsville, Maryland 20705

January 28, 2000

Dear Participant:

Welcome to the combined Animal Genomes, Germplasm, Reproduction & Development and Animal Production Systems National ProgramsWorkshop. I appreciate your willingness to participate in this important effort to shape the agenda for future Agricultural Research Service (ARS) research on Animal Production.

This workshop is designed to gather your input and suggestions for the future directions of these two National Programs. As you may already know, ARS is conducting a series of these workshops in conjunction with the development of 5-year research plans for each of our 23 National Programs. The workshops are designed to hear from you in open forum and to gather your ideas regarding future research directions in this important area of our National Programs.

Your input as an ARS customer, stakeholder, partner, or scientist is critical to shaping the future direction of these important research programs and is, therefore, of great value to us. If you are an ARS **partner, customer, or stakeholder**, I charge each of you to be candid and forthright in sharing your thoughts on the future research agenda. If you are an ARS **scientist**, your charge is to listen. This workshop is a special opportunity to hear first hand the research needs identified by the participants. Your creativity, input, and insights will be of tremendous importance in the next stage of the process as we develop the research action plan.

It is my hope that the exchange and collaboration during this session will further our working relationships. You will all play a valuable role in shaping the ARS national research agenda. The more we communicate with you and you with us, the more successful our ARS program will be overall. This ongoing communication cycle is imperative to our future success and to the future of agricultural research.

Thank you all for taking the time from your busy schedules to be with us during the workshop. Your participation and your ideas are shaping the future of ARS as we move toward the 21st century. Work hard! Best wishes for a successful meeting. Once again, thank you.

Sincerely,

K. Darwin Murrell

K. DARWIN MURRELL
Deputy Administrator

ARS National Program Planning Workshop for Animal Genomes, Germplasm, Reproduction and Development and Animal Production Systems

February 1, 2 and 3, 2000
College Park, Maryland

Holiday Inn
10000 Baltimore Avenue
College Park, MD

February 1, Day 1

7:30 - 8:30	CONTINENTAL BREAKFAST AND REGISTRATION
8:30 - 8:45	WELCOME AND NATIONAL PROGRAM INTRODUCTION Dr. Caird Rexroad, Associate Deputy Administrator
8:45 - 10:00	GUEST SPEAKER- *Topic: "Future production issues for animal agriculture"*
10:00 - 10:15	BREAK
10:10 - 11:00	NATIONAL PROGRAM 102: Animal Production Systems Dr. Lewis Smith, National Program Leader
11:00 - 11:45	NATIONAL PROGRAM 101: Animal Genomes, Germplasm, Reproduction, and Development Dr. Steven Kappes, National Program Leader
11:30 - 1:00	WORKING LUNCH - GUEST SPEAKER- Skip Seward (McDonalds) *Topic: "Development of Animal Food and Fiber Products to meet consumers needs of the future"*
1:00 - 2:15	STAKEHOLDER PRESENTATIONS A representative from each commodity area may present their research problems (25 min. each) Dairy - Steve Larson, Hoard's Dairyman Beef - Terry Klopfenstein, University of Nebraska Swine - Neil Dierks, NPPC
2:15 - 2:30	BREAK

Day 1, continued

2:30 - 3:45	STAKEHOLDER PRESENTATIONS, continued Poultry - John Hardiman, Cobb-Vantress, Inc. Turkey - David Harry, Arbor Acres Farm Sheep - ~~Gregory Lewis, ARS~~ David Green
3:45 - 5:00	OPEN DISCUSSION
5:00 -5:15	ARS Information Staff - Sean Adams
5:15 - 6:15	POSTER SESSION/ SOCIAL HOUR *Research highlights from each ARS center/location*
6:00	ADJOURN

February 2, Day 2

7:30 - 8:30	CONTINENTAL BREAKFAST
8:30 - 8:45	WELCOME AND CHARGE TO BREAKOUT SESSION ONE *Identifying research problem priorities by commodity*
9:00 - 10:30	BREAKOUT SESSION ONE (Dairy, Beef, Swine, Poultry, Sheep)
10:30 - 10:45	BREAK
10:45 - 11:30	REPORT-OUT: RESULTS OF SESSION ONE
11:30 - 11:45	OPEN DISCUSSION
11:45 - 1:00	WORKING LUNCH/ GUEST SPEAKER- Wesley Warren (Monsanto) *Topic: "Impact of Genomics on Animal Research"*
1:00 - 1:15	CHARGE TO BREAKOUT SESSION TWO *Grouping research priorities by problem area*
1:15 - 3:15	BREAKOUT SESSION TWO - Conservation, Characterization and Utilization of Germplasm - Increase Production Efficiency with Genomic Research - Reproductive Efficiency - Nutrition (feed efficiency) - Nutritional Interactions

Research Areas

– research issues for all commodity groups!

Day 2, Continued

3:15 - 3:30	BREAK
3:30 - 4:30	REPORT - OUT: RESULTS OF SESSION TWO
4:30 - 5:00	WRAP-UP, QUESTIONS
5:00	ADJOURN

February 3, Day 3

ARS ONLY

8:30 - 10:00	OPEN DISCUSSION/ FEEDBACK
10:10 - 10:15	BREAK
10:15 - 12:00	BREAKOUT SESSION THREE *Identification of Writing Teams* *Define tasks, dates, and assignments*
12:00	ADJOURN

ANIMAL GENOMES, GERMPLASM, REPRODUCTION & DEVELOPMENT

Program Rationale:
Productions of foods derived from animals has a major impact on the U.S. agricultural economy. Annual cash receipts of $93 billion from livestock and poultry products account for about 50 percent of the receipts from all agricultural products. Identification and use of livestock and poultry with appropriate genotypes will have a major impact on quality of animal products used for food, international competitiveness, and efficiency of production.

Program Components

Animal Germplasm - A major goal is to identify, facilitate, acquire, and characterize potentially useful germplasm, and to conduct animal crossbreeding and selection research to improve efficiency of production and to retain genetic diversity of animals for future generations. Another major goal is to store gametes or embryos on a long-term basis, i.e. 25 years or more. The research effort emphasizes germplasm cryopreservation and vitrification to enhance the feasibility and efficiency under which desired germplasm would be stored. The program includes research on the sexing of male and female sperm so as to provide sexed gametes and embryos for storage. It also includes research on stem cells, primordial germ cells, cell lines, and DNA as they relate to the overall objective of the national program.

Animal Genome - A major goal is to develop genomic maps and associated DNA markers to improve accuracy of selection, increase frequency of desirable genes in populations, and characterize valuable germplasm populations. For each livestock species, genetic maps of polymorphic loci must be developed with sufficient resolution to permit location, definition, and use of genes affecting economically important traits. Related program components include analyses of the fine structure of candidate genes and gene families, definition of the genetic basis of quantitative trait loci to be used to implement genetic marker-assisted selection, and development of new experimental technologies for utilization of genome information.

Reproductive Efficiency - The overall goal is to improve reproductive efficiency of livestock, poultry, and aquaculture species. Research will focus on improving reproductive performance of animals through genetics, nutrition, health management, and on management of environmental factors such as temperature and humidity. Research advances and new biotechnologies will be developed to reduce losses due to reproduction problems in all species, and to maximize reproductive output of animals that produce high quality products.

National Animal Germplasm Database - The overall goal is to develop a fully operational national animal germplasm database system that will be linked with the ARS central and satellite database has been established and is now part of the USDA-ARS Genetic Resources Information Network (GRIN) system at, Beltsville, Maryland. The existing database is on the World Wide Web and is publicly accessible through the Internet at http://www.ars-grin.gov/nag. An important component of the

program is to expand the database to contain descriptors and characteristics of the world's animal genetic resources and DNA sequences or mapping information on relevant animal genomes. An additional program component is development of cooperative arrangements with outside groups such as the National Association of Animal Breeders (NAAB) and the American Livestock Breeds Conservancy to fully develop the database and to establish, for each species, national species committees representing industry scientists and commodities.

Animal Gene Bank/Repository - The purpose is to develop long-term storage space for sperm, embryos, oocytes, stem cells, cell lines, and DNA from designated genotypes covering a wide range of domestic animal species and aquaculture. An important component of this program is to establish a national committee on cryopreservation to work with species committees. This national committee will establish priorities for genetic material to be maintained in repositories, and to define long-term storage requirements for this material.

Projected Outcomes/Impacts of Program Over Next 5 Years

- Complete identification of genes or gene markers related to at least 10 production or disease traits.
- Improve ARS sperm sexing technology by 200-400 percent, to yield sufficient sexed sperm to inseminate 100 cows and 20 sows per day; develop deep freezing methods for sexed sperm.
- Improve cryopreservation by vitrification of embryos in swine to produce live young on a routine basis. Develop preservation technology for swine oocytes.
- Increase lean and decrease fat by at least 10 percent in meat producing beef and swine species and by at least 5 percent in poultry.
- Increase liquid semen storage time from current maximum 6 hours to 48 hours in turkeys and develop frozen semen technology to permit use in turkeys on a practical basis.
- Enhance frozen semen technology in swine for use on a practical market hog production basis.
- Improve in vitro embryo production technology (two to threefold) for efficient production and transfer of sexed embryos in swine and cattle; provide non-surgical embryo transfer technology for swine.
- Develop means to inseminate swine with less than 10 percent of the current number of sperm in an AI dose for swine.

National Program Team Members

Steven M Kappes (leader) - Animal Production/Germplasm

Vacant (co-leader) - Genomics

Linda L Logan Henfrey - Animal Health

Henry S Parker - Aquaculture

Lewis W Smith - Animal Nutrition

National Program Components and Locations

	Program Components				
Locations	Animal Germplasm	Animal Genome	Reproductive Efficiency	National Animal Germplasm Database	Animal Gene Bank/ Repository
Ames, IA					
Athens, GA					
Beltsville, MD					
Brooksville, FL					
Clay Center, NE					
Columbia, MO					
Dubois, ID					
East Lansing, MI					
El Reno, OK					
Fargo, ND					
Fort Collins, CO					
Miles City, MT					
Pullman, WA					
Wyndmoor, PA					

ANIMAL PRODUCTION SYSTEMS

Program Rationale:
Producers are challenged with integrating knowledge from diverse disciplines into production practices suitable for their individual operation. Research on food animal production systems assesses the interactions between nutrition, genetics, reproduction, physiology, microbiology, immunology, and molecular biology, and also related effects on animal health, productivity, and impacts to the environment. Improvements in the production efficiency of individual components are often realized in the total system, and ensure a continuing supply of economical nutrient-dense products for the consumer. Research leading to discoveries and applications in production efficiency, sustainability, animal and environmental well-being, and high quality products are imperative if animal agriculture is to be economically viable.

Program Components

Animal Nutrition - Nutrition is the single most costly component in modern animal production. Suboptimal nutrition is a significant factor in the failure to realize genetic potential for production and increased susceptibility to disease. Economically optimizing nutrient supply and use is imperative for improving growth and reproduction, and to maximizing overall production efficiency. Research is needed in the following areas to improve animal nutrition: 1) chemical composition and availability of nutrients in feedstuffs, 2) nutritional requirements of grazing and non-grazing animals, 3) more efficient use of nutrients, 4) special attention to improving the use of environmentally-sensitive nutrients such as phosphorus, nitrogen, copper, and potassium, and 5) increase understanding of nutrient partitioning between biological functions. (e.g., reproduction, growth, and lactation).

Integrated Animal Systems Research - Production output and efficiency of the whole animal represent the biological integration of nutritional, physiological, and genetic components. Factors that affect an individual component influence animal production, either partially or totally, through their effects on other biological components. It is imperative that research is conducted that develops our knowledge of how animals integrate nutrition, endocrinology, immunology, and genetic factors to optimize efficiency of nutrient use, reproduction efficiency, and product quantity and quality. With this knowledge, we can understand the animal as a production unit in developing new approaches and decision aides applicable to improving the sustainability of animal production systems.

Integrated Information for Animal Production Systems - The overwhelming amount of information about animal production efficiency is difficult to use without the aid of computer-based technology. This technology application is needed to improve management decisions and strategies which will yield the greatest economic return. A feed-composition database is needed to store data critical for sound animal nutrition. Data are needed on differences and trends in feedstuff nutrient content by region, climate, and plant variety. Computer models will contribute to identifying gaps in scientific knowledge. New generation computer models are needed for evaluating production options. Decision-aids are needed that integrate the components of animal production in modular formats that are compatible with farming systems programs.

These decision-aids must be useful to farmers and producers.

Projected Outcomes/Impacts of Program Over Next 5 Years

- Information useful in assembling improved animal production systems.
- Reduced cost systems for managing replacement animals for the breeding herd.
- Improved animal production components for use in whole farm production models.
- Improved definition of dietary nutrient needs for food animals.
- Information on improved sources of nutrients and their bioavailability.

National Program Team Members

Lewis W. Smith (leader) - Animal Nutrition

Steven M. Kappes - Animal Genome

Vacant - Rangeland, Pasture and Forages

Jane F. Robens - Food Safety and Health

Robert J. Wright - Soil Management

National Program Components and Locations

Research under this program is ongoing at many different locations to account for climatic, regional, and geographical variations, as well as many different combinations of germplasm, feeds and management practices, each with unique problems calling for unique research approaches and solutions. Managing these research projects to ensure complementarity and coordination are key roles of the National Program Staff.

	Program Components		
Locations	Animal Nutrition	Integrated Animal Systems Research	Integrated Information for Animal Production Systems
Beltsville, MD			
Booneville, AR			
Brooksville, FL			
Clay Center, NE			
Dubois, ID			
El Reno, OK			
Ithaca, NY			
Madison, WI			
Miles City, MT			
St. Paul, MN			

Customer and Stakeholder

Priority Statements

From: Paula England <pengland@iwaynet.net>
To: NPS.PONPS(AJO)
Date: 1/19/00 11:47AM
Subject: Animal Genetics Workshop

Additional suggestions for ARS Research submitted to me by one of our California members.

1. Further research into protozal based disease processes in cattle (neosporosis, coccidiosis).
   How does the bovine immune system respond?
   How can we improve this response?
   More information on life cycles (particularly neosporosis).
   More information on therapeutic intervention.

2. Lameness issues in dairy cattle.
   What are the relative contributions to lameness problems of:
   A. confirmation
   B. nutrition
   C. environment
   Lameness seems to becoming a major limiting factor in cattle productivity and longevity.

3. The genetic basis for disease resistance.
   Can be breed or engineer for better immune systems?
   Can resistance to specific pathogens or inflammatory mediators be influenced?

4. Identification and long-term preservation of specific germplasm is very relevant to the future progress of genetic improvement while conserving the past. Selection for desirable traits and expediting productive usefulness enables resourceful genetic expectations and potential economic gain. With the near completion of the human genome, related programs in the animal sector will obviously advance. Genetic selection will one day include deliberate accuracy in achieving desirable traits. An immediate area of importance in the dairy industry is in identifying specific milk protein genotypes. Total milk protein concentration and milk protein composition are critical in determining cheese volume and yields. To date, feeding dairy cows* diverse diets have a minimal effect on milk protein traits. Therefore, future modification of milk protein yields and composition must gain scientific support. Further knowledge on specific milk protein genes (alleles on primary chromosomes) and genotype expression merits immediate attention.

Calvin Covington
American Jersey Cattle Association

Babcock

January 26, 2000

Dr. Steven M. Kappes
National Program Leader
Animal Genomes, Germplasm, Reproduction & Development
USDA
ARS
5601 Sunnyside Avenue
Beltsville, MD 20705-5138

Dear Dr. Kappes,

ISA Babcock, a Primary Breeder of Egg laying stocks located in Ithaca, NY, is a member of the Hubbard ISA group. ISA Babcock definitely benefits from the research findings of the USDA/ARS researchers.

Dr. Janet Fulton recently informed me that the ARS is convening a National Program Planning Workshop for the Agency's Animal Genomes, Germplasm, Reproduction & Development and Animal production systems programs.

As a stakeholder of the ARS, ISA Babcock supports the appropriateness of the ARS's research program activities as outlined for discussions at the workshop. The Poultry Breeding industry needs more focused research on: 1) the development of Genomic maps of all poultry species, particularly chickens and turkeys. 2) Genetic makers in candidate genes for resistance to various pathogens. 3) How the Genomic maps could be applied to make genetic improvements in poultry. 4) Cryoppreservation of sexed chicken and turkey embryos.

We are aware that these areas of research require more funding than you are currently allocated and we support your efforts for more funding from the federal Government.

Sincerely,

George A. Ansah, Ph.D.
Director of Research
ISA Babcock

ISA BABCOCK
A DIVISION OF ISA BREEDERS, INC.
P.O. BOX 280 ITHACA, NY 14851-0280
PHONE: 607 272-5990 FAX: 607-272-5998

From: Calvin Covington <CCovington@compuserve.com>
To: National Workshop <ajo@ars.usda.gov>
Date: 1/11/00 11:28AM
Subject: Response

The following is my list of challenges that ARS should address:

1. Economic impact of inbreeding. Need more current data on how inbreeding impacts milk production, calf mortality, reproductive performance, health, etc.
2. Overall herd management. User friendly economic models that will help dairy farmers make better economic decisions. Decisions such as whether to expand or when all factors are considered what is the most productive milk level.
3. Biotechnology. Gene mapping, gene splicing, genetic engineering to produce animals with disease resistance or ability to produce milk for specific uses.
4. Milk components. Research into new uses for milk components. Whey research has produced significant economic benefits to dairy producers. The milk price would be much lower if whey was still dumped and not further processed.
5. Genetic evaluations. Continue to improve and update.

Calvin Covington
American Jersey Cattle Association

From: Dean Danilson <Dean.Danilson@IBPINC.com>
To: "'AJO@ARS.USDA.GOV'" <AJO@ARS.USDA.GOV>
Date: 1/14/00 10:51AM
Subject: Genomes Meeting

As Requested - "most critical problems to be addressed by ARS programs"
(from my perspective)

* Consumer Education & Public Relations
* Meat Quality Effects or Improvements
* Animal Production - Efficiency Improvement

Dean Danilson
IBP, inc.

From: Ben McDaniel <Ben_McDaniel@ncsu.edu>
To: NPS.PONPS(AJO)
Date: 1/14/00 1:01PM
Subject: Critical problems for ARS for Feb. 1-2 meeting

These are my 3 most important:

1. develop or identify the most economical but effective of minimixing soil and water pollution from animal wastes

2. improve genetic evaluation of dairy bulls for production, longevity and disease resistance

3. improve and validate the most effective method of combining genomic and performance informance for genetic evaluation of animals

Ben McDaniel

Priorities for ARS Workshop on Animal Genomics, Germplasm, Reproduction & Development and Animal Production Systems

Kenneth E. Olson, Ph.D.
Dairy and Animal Health Specialist
American Farm Bureau Federation

The following are suggested priority issues in the two national program areas to be discussed:

Integrated Animal Systems

Determine the impact of, and identify ways to improve, current and alternative production systems relative to animal well-being, efficiency and food quality. Animal handling systems, transportation and slaughter should also be evaluated for their impacts. Results of this research must be communicated to farmers and ranchers along with technology needed for the implementation improvements that are identified.

Reproductive Efficiency

Two areas of concern identified by our producers are work on reducing or eliminating Neospora abortions and evaluating the safety of progesterone implants for improved reproductive performance.

Animal Nutrition

Improved estimates of nutrient needs and nutrient intake for all classes of animals to increase production efficiency and minimize the nutrient content of animal manure.

Animal Genome

From a producer standpoint, we are concerned that access to information on the animal genome be available to the public sector. Access to this information is critical to assure that USDA and other public sector researchers have the opportunity to address issues of importance to producers. We encourage utilization of animal genomic information to develop improved diagnostics and therapeutics for use in all species. Diseases for which our producers have identified these needs include Johne's, tuberculosis, transmissible spongiform encephalopathy and trichina. Improved methods of marker assisted selection for enhanced productivity, health and well being is also encouraged.

Gene Bank/Repository

With the widespread use of artificial insemination and a variety of newer technologies in many species, we have a significantly decreased effective population size. This can present problems for a variety of reasons such as the evolution of new diseases or changes in production systems. As a safeguard for the industry, it is critical that we maintain a repository of genetic material.

Easy access to research results by producers and their advisors is also critical. Assuring that project reports and updates are included in the Current Research Information System (CRIS), and that this system continued to be improved in its "user-friendliness is critical. Interaction with the Agricultural Databases for Decision Support program to assure inclusion of the latest research results is also strongly encouraged.

PIC

PIC
2929 Seventh Street
Suite 130
Berkeley, CA 94710
Phone (510) 848-8266
Fax (510) 848-0324

January 5, 2000

Dear Amy,

Feb 1-2, ARS workshop in College park

5 Critical problems for ARS to focus on:
1) IVP in pigs
2) Use of human genomic information for application in agricultural species
3) Acceptability of biotechnology in the food chain
4) Environmental pollution
5) Food safety and meat quality

Dr Hein van der Steen
Director of Animal Science Research
PIC Group

WHEELER BROTHERS GRAIN COMPANY
INCORPORATED

Telephone: (580) 623-7265 Fax #: (580) 623-2343
P.O. Box 29 • Watonga, Oklahoma 73772

Grain Merchants - Cattle Feeders - Since 1917

From: Steve Smola

1. Feed efficiency through improved genetics and also through nutrition, especially from various nutritional backgrounds. Example: Cattle from New Mexico US cattle from Florida.

2. Develop genetics and nutrition for quality and consistent of end product.

DEPARTMENT OF HEALTH & HUMAN SERVICES

Public Health Service

Food and Drug Administration
Rockville MD 20857

JAN 21 2000

Dr. Steven M. Kappes, National Program Leader
- Animal Genomes, Germplasm, Reproduction & Development
Dr. Lewis Smith, National Program Leader
- Animal Production Systems
United States Department of Agriculture
Agriculture Research Service
5601 Sunnyside Avenue
Beltsville, Maryland 20705 - 5138

Dear Drs. Kappes and Lewis:

As requested in your December 14, 1999 letter, I am offering for your consideration several critical problems that might be effectively addressed within your programs at the ARS National Program Planning Workshop on February 1-2, 2000.

1. Risk assessment to predict establishment and environmental effects of escaped genetically engineered aquaculture organisms.

   Importance: Researchers in genetic engineering of aquaculture species, for example Atlantic salmon, are on the threshold of producing commercially available strains of fish with improved growth rates and feed efficiencies. While attempts will be made to prevent escape of these new transgenic strains into the environment, it is unlikely that biocontainment will be absolutely successful. A precondition for the successful large-scale commercial introduction of bioengineered species into aquaculture is a detailed risk assessment model for assessing individual bioengineered strains for their potential to be accidentally established in the environment. A further step would be a systematic, ecosystem-specific methodology to predict the potential impacts of such an establishment on native aquatic populations, including gene introgression into wild populations.

2. Criteria and plans are needed for monitoring and evaluating the long-term safety (animal safety and food safety) of combinations of transgenes added to food-producing animal breeds.

   Importance: Germ-line transgenic animals of domestic, food-producing species are soon to be a reality in commercial agriculture. Bioengineered varieties under development by diverse research institutions contain a variety of small, heritable gene additions, usually designed to improve growth. Business models for developers of such transgenic animals, cattle for example, include the sale of semen from transgenic bulls to cattlemen throughout the country. Thus, introgression of transgenes into the general cattle population could occur rapidly and with relatively little ability to track their effects as, with further generations, combinations of transgenic constructs occur. The costs of removal of a combination of transgenes with unforseen adverse effects from one domestic breed of cattle could be considerable, if the industry is not prepared for such an eventuality. Breed associations need assistance in deciding under what conditions a transgenic animal, especially a bull, can be registered as a "purebred." What performance characteristics are to be monitored in the daughters and sons of

transgenic sires? Will or can a non-engineered line be preserved within the breed? What is the breed registry status of animals carrying multiple transgenic constructs? Should all breeds conform to the same standard? If so, should it be a national or international standard? If breed registries decide not to register transgenic animals, how may they be efficiently tracked and evaluated?

3. Criteria for evaluating the safety of vectors and markers used in gene therapy and DNA vaccines.

Importance: Gene addition through somatic cell therapy is often accomplished by means of a viral vector that inserts the genetic construct into the target cells. Some of the vectors in experimental use are replication-deficient human and animal pathogens; often those developed for unrelated human gene therapy experiments. The safety of these various vectors to target animals, domestic animal populations and in food derived from these animals has not been rigorously evaluated. The same can be said for various marker genes/proteins, e.g., green fluorescent protein, used to show successful gene incorporation. Criteria for systematically evaluating various gene vector and marker systems for animal and food safety are needed. For example, what factors influence the potential for crippled vectors to be recombined into competent pathogens of animals or man? What are other potential risks and how may they be evaluated prior to large-scale commercial use in animal agriculture? Are some vectors and markers inherently safer for use in some species? Are some vectors and markers safer for the production of animal-derived food for humans?

Thank you again for your consideration of these issues.

Sincerely yours,

SFSJ

Stephen F. Sundlof, D.V.M., Ph.D.
Director, Center for Veterinary Medicine

HY-LINE INTERNATIONAL
RESEARCH DEPARTMENT

2583 240TH STREET. P.O. BOX 310
DALLAS CENTER, IOWA 50063
PHONE (515) 992-4173 • FAX (515) 992-3203

January 17, 2000

Dr. Steven Kappes
National Program Leader-Animal Genomes,
Germplasm, Reproduction & Development
5601 Sunnyside Ave.
Betlsville, MD 20705-5138

Dear Dr. Kappes,

Hy-line international is pleased to be invited to provide input to the USDA/ARS National Program planning Workshop to be held Feb. 1 and 2, 2000.

Below is outlined several critical problems that need to be addressed by the ARS program.

1. Genome mapping
A major goal of the ARS National Program is to develop genomic maps and associated DNA markers to improve overall selection efficiency in the industry. ARS scientists spearheaded the effort to develop the chicken genome map. International collaborations were subsequently established with the result that the chicken genome map now contains approximately 2000 markers. Development of marker kits and their subsequent release to interested scientists has really "jump-started" the poultry genome mapping efforts.

However, the current ARS efforts in poultry gene mapping consist of 0.9SY with less than $18,000 discretionary funds. This is not even close to adequate to continue the genome mapping efforts. Resistance to diseases is one of the most difficult traits to measure and yet has the greatest potential for gain. Marek's disease virus continues to mutate and cause severe economic losses to the industry. Salmonella is of great concern to both the industry and consumer. Research is needed in understanding the genetic mechanisms of disease resistance in poultry. $18,000 is an inadequate amount to fund this effort.

There is no ARS funding for genome mapping for any other poultry species such as turkey or ducks. Due to gene conservation and genetic synteny across species, such map information will be applicable between agriculturally important avian species. However, the preliminary maps needed are non-existent.

2) Germplasm Preservation
An ARS goal is to develop long-term storage space for sperm, embryos etc to preserve genetic material for future use. At this time, the only practical method of germplasm preservation for poultry is semen cryopreservation. This works fairly well for turkeys, poorly for chickens and does not work for other avian species. There are no methods for ova preservation, embryonic cell preservation yields less than 0.25% recovery and there are no methods for cloning of avian somatic tissues. Semen preservation does not allow regeneration of a pure line. This is a critical deficiency for the poultry industry. We need methods for preservation of existing genetic resources before they are irretrievably lost.

Several institutions in the US and Canada are maintaining rare poultry stocks and genetic resources through live animals. In the past 15 years, there has been a loss of 37% of the poultry genetic stocks held at public institutions (almost half of this loss occurring within the past 4 years). Approximately one-third of the remaining stocks are considered to be at high risk of elimination within the next few years due to severe budgetary constraints. Many of these stocks represent gene pools of the past that are no longer represented in the commercial strains used today. The poultry industry needs to be able to access these gene pools to meet future changes in consumer demands.

There are also unique mutation stocks and selected genetic lines that contain genetic variation that would be either impossible or extremely expensive to regenerate. With the new techniques of molecular biology and the developing avian genomic maps, we can now begin to access these genes and gain a better understanding of embryonic development, genetic interactions and quantitative trait loci influences. Until the industry has consistent and reliable methods of cryopreservation we need to ensure that the existing avian genetic resources are conserved.

I look forward to meeting with you Feb. 1 and 2.

Sincerely,

Janet Fulton

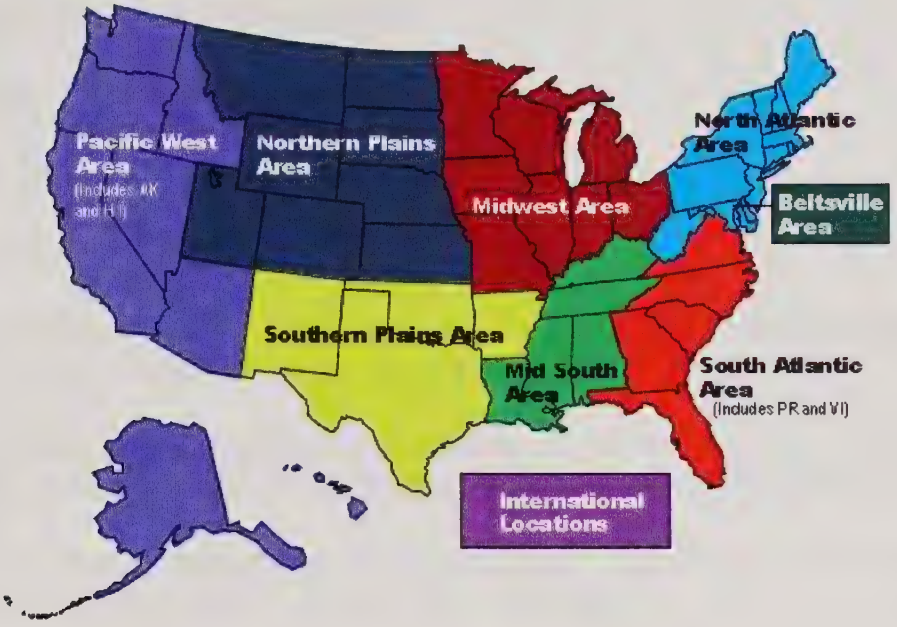
Janet Fulton, PhD
Molecular Biologist

ARS National Program 101

Research Areas and Project Locations

ARS Research Locations for the National Program for

Animal Genomes, Germplasm, Reproduction & Development



Beltsville Area — Livestock & Poultry Sciences Institute, Beltsville, MD
(http://www.lpsi.barc.usda.gov/)

Midwest Area — Animal Physiology Research Unit, Columbus, MO
(http://www.agron.missouri.edu/ars_columbia/apru.html)
Avian Disease and Oncology Laboratory, East Lansing, MI
(http://www.msu.edu/~arsadol/)

North Atlantic Area — Eastern Regional Research Center, Wyndmoor, PA
(http://www.arserrc.gov/)

Northern Plains Area — Plant Germplasm Presevation Research Unit, Ft. Collins, CO
(http://checkers.nssl.colostate.edu/research/reserh1.html)
Fort Keogh Livestock and Range Research Laboratory, Miles City, MT
(http://larrl.ars.usda.gov/)
U.S. Meat Animal Research Center, Clay Center, NE
(htttp://www.marc.usda.gov/marc/html/marc.html#MARC)

Pacific West Area — U.S. Sheep Experiment Station, Dubois, ID
(http://pwa.ars.usda.gov/dub/index.html)

South Atlantic Area — Beef Cattle Research Unit, Brooksville, FL
(http://www.ifas.ufl.edu/~starsweb/)
Southeast Poultry Research Laboratory, Athens, GA
(http://seprl.ars.usda.gov/)

REGULATION OF OVARIAN FOLLICULAR DEVELOPMENT IN BEEF CATTLE

Project: 5438-31000-046-00D

Location: Clay Center, Nebraska

Researchers: S. Echternkamp

Objectives:

(1) Identify genomic markers (quantitative trait loci, QTL) for genes regulating critical components of ovulation and breeding performance of beef cattle.

(2) Identify candidate genes linked with phenotypic variation in ovarian follicular development, ovulation rate and conception among selected populations of cattle.

(3) Develop production systems and procedures to reduce dystocia and retained placentae and to increase calf survival in beef cattle.

Approach:

To identify rate limiting processes associated with conception failure in beef cattle, DNA will be isolated from tissue of cattle with diverse reproductive performance (e.g., MARC twinner cattle) and screened with microsatellite markers to identify genomic alleles linked to phenotypic differences in ovarian follicular development, ovulation and fertility. Identified genomic markers (QTL) will be assigned to regions of chromosomes using the MARC bovine linkage map. Candidate fertility genes will be identified either by association with known genes in the same region of the chromosome(s) as the markers or by DNA sequencing of marker regions. Animal experiments will correlate molecular, biochemical and/or physiological differences in expression of identified candidate genes with differences in reproductive performance. Associations among gestational length, dystocia, calf survival, retained placenta, nutrition and conception will be used to develop production systems to reduce dystocia, calf mortality and postpartum infertility and to enhance reproductive efficiency.

OVARIAN FOLLICULAR DEVELOPMENT AND OVULATION IN BEEF CATTLE

Project: 5438-31000-047-00D

Location: Clay Center, Nebraska

Researchers: A. Roberts

Objectives:

(1) Identify molecular, biochemical, and endocrine processes controlling follicular development and ovulation in beef cattle.

(2) Determine physiological processes by which genetic and environmental factors influence follicular development and ovulation.

Approach:

Ovarian follicular development is a prerequisite for determining age at first conception, interval between conceptions, and total number of calves produced by a cow. Understanding the physiological parameters controlling follicular development and the processes by which genetic and environmental factors influence these parameters is essential to increase efficiency of beef cattle production. The overall hypothesis of the project is that follicular development and ovulation are regulated by complex interactions among circulating hormones and factors (steroids and proteins) produced within individual follicles and that these interactions are modulated by genetic and environmental influences. Experiments will 1) determine molecular, biochemical, and endocrine processes controlling follicular development and ovulation and 2) identify physiological traits associated with genetic and metabolic influences on follicular development and ovulation. This information is required to develop management and genetic strategies to improve reproductive efficiency of beef cattle.

FINE MAPPING OF QUANTITATIVE TRAIT LOCI IN LIVESTOCK GENOMES

Project: 5438-31000-038-00D

Location: Clay Center, Nebraska

Researchers: T. Smith
S. Fahrenkrug

Objectives:

(1) Develop informative markers in the vicinity of mapped quantitative trait loci (QTL) to increase accuracy and resolution of mapping and to provide a marker pool, that increases the probability of informativeness in commercial breeding populations.

(2) Identify candidate genes for the QTL.

(3) Evaluate positional candidate genes for effect on QTL.

Approach:

Markers associated with trait variation will be used to screen Yeast Artificial Chromosome (YAC) libraries to obtain additional linked microsatellite markers. These markers will be immediately used to increase the number of informative meioses in the resource population,verifying the initial mapping results and increasing the resolution. Local comparative maps to human and mouse genomes will be produced, and genes on the maps of these species will be used to produce gene markers closely linked to the quantitative trait loci (QTL). Candidate genes will be selected from the human and mouse maps on the basis of plausibility with regards to the trait under consideration, or generated by RNA-based difference analysis of tissues from animals at extremes of the phenotypic ranges. Candidate genes showing no recombination with the the QTL will be selected for expression studies in other populations to verify effect. QTL genes will then by analyzed at the cDNA sequence level to determine the basis of the variation.

GENETIC CHANGE IN CALVING EASE AND QUANTITATIVE TRAIT LOCI DETECTION IN CATTLE POPULATIONS

Project: 5438-31000-048-00D

Location: Clay Center, Nebraska

Researchers: G. Bennett
J. Keele
E. Casas
R. Thallman

Objectives:

(1) Estimate genetic change in calving ease of two-year-old heifers resulting from seven years of selection.

(2)Evaluate genetic changes in correlated traits to identify useful indicator traits and possible problems with this method of selection.

(3) Identify quantitative trait loci (QTL) for important meat, ovulation, and production traits in beef cattle.

(4) Develop methods to find QTL in existing cattle populations.

(5) Use selection herds to validate QTL effects and evaluate their potential use in beef cattle improvement.

Approach:

Substantial change in calving ease has been made during five years of selection in seven populations of cattle. Complete the final two years of selection for calving ease using multiple-trait genetic prediction methods. Use statistical methods to estimate genetic changes in heifer calving ease, birth weight, weaning weight, yearling weight, gestation length, pelvic area, and calf survival based on data collected while cattle were being selected. Slaughter a sample of steers from select and control lines to evaluate the effects of selection on carcass measurements. Use and develop quantitative methods to identify loci affecting traits within populations. Use a dense genetic marker map to identify quantitative loci in populations of cattle with differences in ovulation rate, muscularity, and meat quality. Structure and plan other populations to validate identified quantitative trait loci. This approach should identify methods that can be used for genetic improvement of livestock.

DEVELOP INFORMATION SYSTEMS FOR MARKER-ASSISTED SELECTION

Project: 5438-31000-049-00D

Location: Clay Center, Nebraska

Researchers: J. Keele

Objectives:

(1) Develop an information system to support marker-assisted selection by identifying and mapping chromosomal regions that influence carcass leanness, meat palatability and reproduction.

(2) Maintain, integrate and distribute data within and between laboratories and species using a database.

(3) Develop efficient techniques for identifying quantitative trait loci (QTL).

(4) Develop marker-assisted selection strategies for the livestock industry.

Approach:

Over the last three years, 1600 progeny sired by four bulls were produced. Carcass leanness, meat palatability and reproduction data were collected. DNA was obtained for the pedigree. Sires were crosses among breeds representing extremes in carcass leanness, meat palatability and reproduction to increase the power of identifying and mapping QTL. Using a few large half-sib families increases the power of identifying specific QTLs at the expense of identifying fewer QTLs. Only those QTLs segregating within the half-sib families can be identified. Genotyping subsets of the population in multiple stages reduces the cost of QTL identification without sacrificing power. Genotyping only extreme animals in the early stages focuses the effort in subsequent stages on a few, specific chromosomal regions. A relational database integrates data between projects and species.

STRATEGIES TO OPTIMIZE CARCASS YIELD AND MEAT QUALITY OF RED MEAT ANIMALS

Project: 5438-31430-001-00D

Location: Clay Center, Nebraska

Researchers: M. Koohmaraie
St. Shackelford
T. Wheeler

Objectives:

(1) Identify and validate genetic markers for carcass composition and meat tenderness.

(2) Develop an instrument procedure to accurately measure tenderness and red meat yield for beef.

(3) Obtain the necessary information to manipulate the systems regulating muscle growth and meat tenderness.

(4) Develop genetic and postmortem strategies to improve red meat yield and palatability.

(5) Evaluate effects of breeds representing diverse biological types on carcass composition and meat quality.

Approach:

Whole-genome linkage analysis will be used to identify genetic markers for carcass composition and meat tenderness. Will use knowledge of biological factors regulating meat tenderness to develop a tenderness-based beef classification system and strategies to improve meat tenderness. Detailed carcass composition and meat quality measurements will be used to evaluate breeds representing diverse biological types. Will utilize mRNA differential display, gene expression fingerprinting, and representational difference analysis of cDNA or other emerging methodologies to identify and characterize genes differentially expressed in callipyge lambs. Will determine the role of the calpain proteolytic system in muscle protein turnover by overexpression of bovine calpastatin cDNA in muscle cell lines and transgenic mice. By identifying and sequencing the calpastatin gene promoter, we will determine how expression of the calpastatin gene is regulated. Some of these experiments will be conducted in biosafety level 2 laboratories.

IDENTIFY QTL FOR MEAT QUALITY IN CATTLE

Project: 5438-31000-030-00D

Location: Clay Center, Nebraska

Researchers: R. Stone

Objectives:

(1) Identify quantitative trait loci (QTL) in beef cattle with emphasis on meat quality and composition.

(2) Increase marker density in regions flanking QTL with major influences so that marker assisted selection (MAS) can be implemented.

(3) Map genes that are candidates for influencing meat quality and composition.

Approach:

Identify QTL segregating in populations of cattle using existing marker-based linkage maps. Phenotypic variation in meat quality, segregating with markers chosen to cover the genome at 15 to 20 centimorgan intervals, will be analyzed initially. Any region of the genome containing QTL with major influences will be further mapped to flanking intervals of 5 centimorgans or less using additional markers from the linkage map. Enrichment of flanking markers necessary for possible implementation of marker-assisted selection or positional cloning will be derived from bovine yeast artificial chromosome clones shown to be contiguous by screening with the markers available. Genes that are possible candidates for affecting meat quality such as those affecting fat deposition will be mapped by traditional methods. Any of these genes that map to the same chromosome region as a phenotype for meat characteristics will become positional candidate genes.

SELECTION FOR LITTER SIZE IN SWINE

Project: 5438-31000-031-00D

Location: Clay Center, Nebraska

Researchers: K. Leymaster
B. Frekling

Objectives:

(1) Evaluate direct and correlated responses to selection for ovulation rate or uterine capacity in swine.

(2) Investigate physiological factors associated with genetic changes in ovulation rate or uterine capacity.

Approach:

Single-trait selection lines for uterine capacity and ovulation rate were started in 1987. Uterine capacity is estimated as twice the litter size at birth of unilaterally hysterectomized-ovariectomized (UHO) gilts. Ovulation rate is measured by laparoscopy at 40 days of gestation. Each selected line uses 36 boars and 100 farrowing gilts per generation, split evenly into two replicates. An unselected control line is maintained with 10 boars and 20 farrowing gilts per replicate. Eight generations of selection are completed. During this period, a terminal evaluation will be conducted to estimate direct and correlated responses to selection. One-half of the gilts of each line will remain intact to measure ovulation rate and litter size, whereas UHO will be imposed on the remaining gilts to measure ovulation rate and uterine capacity. Consequently, the effectiveness of selection for ovulation rate (uterine capacity) and associated changes in uterine capacity (ovulation rate) and litter size can be estimated in the ovulation rate (uterince capacity) line.

GERMPLASM EVALUATION IN BEEF CATTLE

Project: 5438-31000-033-00D

Location: Clay Center, Nebraska

Researchers: L. Cundiff
L. Van Vleck

Objectives:

(1) Characterize breeds representing diverse biological types for a wide spectrum of biological traits contributing to economic beef production.

(2) Evaluate genotype-environment interaction among breeds representing diverse biological types from tropical and temperate regions of the world.

(3) Determine favorable and unfavorable effects of a major gene for leanness on economically important traits in alternative mating systems.

Approach:

F1 cows out by Tuli, Boran, Brahman, Belgian Blue and Hereford and Angus sires and out of Angus, Hereford and MARC III cows are being evaluated for reproduction and maternal performance when mated to Charolais and Belgian Blue F1 sires. F1 crosses produced using semen from the same sires of two or more tropically adapted breeds (Tuli, Boran, or Brahman) are also being evaluated at experiment stations in Florida, Georgia, Oklahoma, Louisiana, and three locations in Texas to assess genotype-environment interaction. Effects of 0, 1 or 2 copies of markers closely linked to the muscle hyperplasia (double muscling) gene will be evaluated in reciprocal backcross and F2 progeny that differ in proportion Piedmontese inheritance (25:75, 50:50, 75:25). F1 progeny by Friesian, Swedish Red and White or Norwegian Red, Wagyu, and Angus and Hereford sires out of Angus, Hereford, and MARC III dams will be produced and evaluated for growth and carcass traits and for reproduction and maternal performance.

IDENTIFY QTL AND DEVELOP GENETIC STRATEGIES TO IMPROVE LEANNESS IN SHEEP

Project: 5438-31000-037-00D

Location: Clay Center, Nebraska

Researchers: K. Leymaster
B. Freking
L. Van Vleck

Objectives:

(1) Identify quantitative trait loci (QTL) affecting growth, carcass leanness, meat tenderness, and reproductive traits in sheep resource populations.

(2) Develop and evaluate strategies to select for lean growth efficiency in a terminal sire composite population.

Approach:

A resource population was produced to achieve segregation of the callipyge allele affecting muscle and fat deposition. Growth, carcass leanness, and meat tenderness traits are being recorded on two replicates of the F2 generation derived from the Dorset and Romanov breeds. Initial genotyping efforts will emphasis microsatellite markers on chromosome 18, the reported location of the callipyge locus. Subsequently, markers evenly spaced over the entire genome will be used. Genotypic and phenotypic data will be analyzed jointly to detect chromosomal segments associated with phenotypic variation. The callipyge allele will also be introgressed into a terminal sire composite population to aid additional studies concerning expression and meat tenderness. Selection for an index combining daily gain and residual feed intake will continue in the terminal sire composite population. The index attempts to increase growth while allowing a slight increase in feed intake.

IDENTIFY AND VALIDATE QUANTITATIVE TRAIT LOCI IN SWINE

Project: 5438-31000-039-00D

Location: Clay Center, Nebraska

Researchers: G. Rohrer

Objectives:

(1) Identify chromosomal regions which affect reproduction, carcass composition and growth traits in swine.

(2) Resolve the estimated position and effect of quantitative trait loci (QTL) by saturating the identified regions with additional microsatellite markers.

(3) Verify selected QTL by mating individuals with different QTL genotypes to observe their progeny's phenotype.

(4) Identify genes which cause the effect observed for verified QTL by using the porcine YAC library.

Approach:

A resource population was developed with Meishan and White Composite pigs. Measurements recorded were weight and backfat thickness at 4 week intervals, age at puberty, carcass composition, and litter size in unilaterally ovariectomized-hysterectomized sows. Microsatellite markers, spaced 15-20 cM apart, will be genotyped across all animals and associations between phenotypes and marker genotypes will be determined across the entire genome. Additional markers in the identified regions will be genotyped to determine the most likely position and the magnitude of the effect for each region. When required, additional markers will be developed through the use of the porcine YAC library. QTL with the most important effects will be verified by mating animals with selected marker genotypes to produce progeny with specific QTL genotypes. These progeny will also be useful to further resolve estimated parameters for the QTL. Genes which cause the observed effect will be identified by implementing a positional candidate gene approach using the porcine YAC library.

GENETIC DISEASE RESISTANCE TO MUCOSAL PATHOGENS IN LIVESTOCK

Project: 5438-32000-015-00D

Location: Clay Center, Nebraska

Researchers: M. Heaton
M. Chitko
W. Grosse

Objectives:

(1) Identify genes affecting infectious disease traits in livestock and develop gene-based technologies for increasing food safety and improving herd health.

Approach:

Newly developed expression-based technologies will be used to identify and map livestock genes that respond to pathogen exposure. These genes will become candidates for gene-based interventions and, in turn, facilitate the targeting of relevant pathways for molecular genetic dissection. Based on similarities with other well-studied mammalian systems, targeted livestock pathways provide a relevant source of novel candidate genes. The association of candidate gene alleles with infectious disease phenotypes will be evaluated in genetically diverse herds of intensively and extensively managed livestock. Identifying genes that affect disease resistance will provide opportunities for a variety of interventions.

THE ADIPOSE TISSUE - BRAIN - PITUITARY AXIS

Project: 6612-31000-011-00D

Location: Athens, Georgia

Researchers: G. Hausman
C. Barb

Objectives:

(1) Elucidate endocrine regulation of preadipocyte recruitment and proliferation.

(2) Identify growth factors, binding proteins and transcription factors involved in fetal adipogenesis.

(3) Immunize animals against adipose lineage cells.

(4) Characterize expression of leptin and leptin receptor and serum leptin concentrations as influenced by age, sexual dimorphism and metabolic fuels.

(5) Determine the role of leptin and neuropeptide-Y in regulating hormone secretion.

Approach:

Developmentally regulated proteins will be examined with Western and Northern blots, immunocytochemistry and in situ hybridization techniques. Function & mode of action of primary factors in adipose tissue development will be examined in normal, hypophysectomized, and hormone supplemented fetuses. Differentiation of stromal vascular cells from experimental fetuses will be assessed in primary cell cultures. Preadipocyte commitment and differentiation will be studied in cultures either depleted or enriched for preadipocytes. Effects of intracerebroventricular or peripheral administration of leptin on GH and LH secretion will be studied. Influence of metabolic fuels on leptin expression and secretion will be determined using metabolic inhibitors. In vitro studies using pituitary cell culture and hypothalamic perfusion will be used to assess influence of leptin and neuropeptides on regulation of GH and LH secretion from the pituitary. In situ hybridization will be utilized to quantify brain leptin receptor level after exposure to neuropeptides.

BRAIN MATURATIONAL PROCESSES WHICH FORM THE LUTEINIZING HORMONE PULSE GENERATOR

Project: 6612-31320-001-00D

Location: Athens, Georgia

Researchers: R. Kraeling

Objectives:

(1) To determine the ontogeny of the brain maturational processes which culminate in formation of and peripuberal function of the luteinizing hormone pulse generator and peptidergic pathways which enhance or limit these processes.

Approach:

Studies will be conducted throughout the prepuberal and peripuberal periods. The following will be examined in gilts raised under standard management conditions: 1) the effect of hypothalamic lesions induced by neonatal treatment with glutamate on age at puberty and response of the LH pulse generator to the following challenges: a) ovariectomy (OVX), b) physiological levels of estradiol and progesterone, c) the endogenous opioid peptide antagonist, naloxone, and d) the excitatory amino acid agonist, n-methyl-D, L aspartate (NMA), 2) the effect of repeated treatment with NMA throughout the prepuberal period on age at puberty, 3) age related changes in sensitivity of the LH pulse generator to the suppressive effects of estradiol and 4) the age at which naloxone will stimulate LH release in progesterone-treated OVX gilts will also be determined. In addition, the effect of confinement and the effect of relocation plus boar exposure on the LH response to the above treatments will be studied.

EVALUATION OF TROPICALLY ADAPTED BEEF CATTLE GERMPLASM IN THE SUBTROPICS OF THE UNITED STATES

Project: 6619-31630-001-00D

Location: Brooksville, Florida

Researchers: C. Chase
S. Coleman

Objectives:

(1) Evaluate tropically adapted beef cattle germplasm in the subtropics of the U.S. by a) Improvement of breeds existing in the U.S. Characterization and evaluation of tropically adapted Bos taurus breeds that have potential for increasing production efficiency, especially reproductive efficiency, and potential for improving marketability.

(2) Preserve valuable beef cattle germplasm by maintaining a repository of frozen semen and embryos of selected breeds adapted to the subtropics of the U.S.

Approach:

1a. Evaluate Brahman sires for genetic variation in tenderness and determine the relationship between this variation and genomic polymorphisms, the expression of key proteases of the calpain/calpastatin system, and other regions of the genome suspected of harboring genetic mechanisms underlying quantitative trait loci (QTL) effects for tenderness. 1b: 1) Evaluate reproductive and maternal traits of Tuli-, Senepol-, and Brahman-sired females; 2) Determine heterosis between the Bos taurus breed, Romosinuano, and Angus and Brahman cattle; 3) Develop a precise systematic scheme, based on DNA markers, to characterize breed diversity and within breed variability among tropically adapted breeds of beef cattle; 4) Determine the mechanisms involved for adapted breeds to withstand the stresses of subtropical environments; and 5) Determine the potential for future U.S. beef cattle evaluations to include the Caracu breed native to Brazil and/or the Africander breed native to South Africa. 2: As breed evaluations are terminated, preserve germplasm as semen and embryos for future research.

IDENTIFICATION AND MANIPULATION OF GENETIC FACTORS TO ENHANCE MILK PRODUCTION AND QUALITY

Project: 1265-31000-067-00D

Location: Beltsville, Maryland

Researchers: R. Wall
A. Capuco

Objectives:

(1) Elucidate genetic mechanisms that control mammary gland growth, development, function and apoptosis (involution). That basic information will be used to develop genetic engineering strategies for modifying milk composition to improve manufacturing properties, and generate new animal products.

Approach:

Histological, cell physiology and recombinant DNA techniques will be used to quantify secretory epithelial cell turnover during lactation and determine the underlying basis for the decline in milk yield during lactation in the bovine. Recombinant DNA methods will be used to clone and fabricate inducible mammary gland specific gene constructs consisting of various regulatory elements and structural genes. The resulting transgenes, designed to increase milk value, will be screened in transgenic mice and those with the most promise will be introduced into goats. Mammary gland function, cell physiology, gene regulation and physical chemical properties of milk from the transgenic goats will be studied.

MOLECULAR BASIS FOR IMPROVED MILK PROTEIN BASED DAIRY PRODUCTS

Project: 1935-31440-002-00D

Location: Wyndmoor, Pennsylvania

Researchers: H. Farrell, Jr.
P. Hoagland

Objectives:

(1) To elucidate the basic milk protein structural motifs responsible for protein-protein interactions in milk and dairy products.

Approach:

Structural predictions of previously developed computer assisted molecular models of milk proteins will be tested experimentally by determination of protein structural motifs altered in response to environmental effects. Specifically, effects of changes in salt, water and sugar content on development of new patterns of intra- and inter-molecular associations of milk proteins will be studied by sophisticated instrumental techniques capable of providing information on secondary, tertiary and quaternary structure and side-chain configuration; this will cast new light on these complex interactions which, when altered by the environment, have a major influence on the textural character of the foods made from them. This database of interesting structural features of, among others, peptide segments of individual proteins, may then be used to provide a fundamental explanation of results observed during such processes as yoghurt or cheesemaking. This information will be supplemented by studies of environmental factors influencing protein folding, micelle assembly and secretion in vivo.

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PHYSIOLOGICAL MECHANISMS OF STRESS AND GROWTH IN NEONATAL PIGS

Project: 3622-32000-003-00D

Location: Columbia, Missouri

Researchers: R. Matteri
J. Carroll

Objectives:

(1) Investigate the effects of production stressors on the neuroendocrine, immune and metabolic systems of neonatal pigs and determine how such effects alter the interaction of these systems and target tissues to limit development, performance and well-being.

(2) Investigate the endocrine mechanisms regulating the stress response and neonatal growth and how such mechanisms are influenced by endogenous and exogenous factors.

Approach:

Experiments will be conducted to investigate the health, performance, and well-being of the baby pig during the postnatal period and determine important regulators and mechanisms of stress and growth. Applied studies will determine factors contributing to the greatest sources of mortality, crushing and chilling, and attempt to identify physiological mechanisms that could be altered or modified to reduce high mortality. Basic studies will investigate the regulation of the hypothalamic-pituitary-adrenal axis using various hormonal, and cytokine challenges and neuroendocrine-immune mechanisms in the brain will be determined. Regulatory mechanisms of growth-related endocrine function pertinent to performance in the presence or absence of stress will be examined in a series of developmental, genetic, and nutritional studies. Various stress and growth regulators, their receptors, their molecular regulation and effect of target tissues will be established using in vitro cell cultures, immuno- and bio-assays,and standard methods for evaluating gene expression.

IDENTIFICATION & CHARACTERIZATION OF QUANTITATIVE TRAIT LOCI RESISTANCE TO DISEASE IN CHICKEN

Project: 3635-31000-005-00D

Location: East Lansing, Michigan

Researchers: H. Cheng
R. Witter

Objectives:

(1) Increase the utility of the chicken genetic map.

(2) Fine-map and characterize non-MHC quantitative trait loci that confer resistance to Marek's disease.

Approach:

To increase the utility of the East Lansing genetic map, additional microsatellite markers will be developed by genotyping polymorphic markers on our 52 standard progeny. Also, comparative anchor reference loci will be mapped to align the chicken genome with the human and mouse genomes by either the use of allele-specific PCR primers or RFLP. To fine-map our QTLs for disease resistance to Marek's disease, recombinant congenic strains (RCS) are under development using the resistant Line 6 and the susceptible Line 7 as parents. Each of the RCS lines will be screen for the QTLs that we have identified. Genotyping the progeny from additional test crosses using each line will enable us to resolve the QTLs to regions 5 cM or less in size. In a separate project, three resource populations developed in collaboration with Agriculture Canada will be screened for QTLs for production traits on chromosomes 1 and 2 using evenly-spaced microsatellite markers.

IDENTIFICATION AND UTILIZATION OF GENES CONTROLLING DISEASE RESISTANCE IN CHICKENS

Project: 3635-31320-005-00D

Location: East Lansing, Michigan

Researchers: L. Bacon
H. Hunt
R. Witter

Objectives:

(1) Identification of non-MHC genes that confer resistance to MD.

(2) Develop methods based on knowledge of MHC genes for optimizing antigen presentation and immune responses to MD and other pathogens.

(3) Use of transgenic methods to determine function of MHC or pathogen-derived genes in disease resistance.

Approach:

A multidisciplinary approach is proposed to define the genetics of disease resistance and immune response. Genetic resistance to Marek's disease and lymphoid leukosis, two different viral induced lymphoid tumor diseases in chickens, is emphasized. In objective 1, individual non-MHC genes with an important influence on Marek's disease will be identified using recombinant congenic strains under development. When desirable individual genes are identified, we will study the function of the molecules they encode and develop reagents for their molecular identification and selection. Objective 2 details this aspect of research for the major histocompatibility complex (MHC or B-complex) genes. B genes have been associated with an important influence on innate and vaccinal immune response to Marek's disease virus utilizing developed B-congenic chickens. Objective 3 involves the adaptation of transgenic technology to further establish the role of individual genes in disease resistance.

INCREASING FLOCK AND EWE PRODUCTIVITY

Project: 5364-31000-006-00D

Location: Dubois, Idaho

Researchers: J. Stellflug
G. Snowder

Objectives:

To relieve range sheep productivity constraints by:

(1) Determining breed response to different environments.

(2) Quantification of changes in growth, composition and puberty; and to extended data in development and refinement of a deterministic simulation model.

(3) Develop selection procedures to increase genetic progess.

(4) Develop cost effective artificial insemination and explore embryonic loss causes. Determine interactions between intake and condition on supplementation.

Approach:

A multidisciplinary approach will be used to study genetic, reproductive physiology, production systems and nutrtional components of sheep biology when different breeds, crossbreds, environments and nutritional conditions are imposed. Utilization and improvement of genetic resources will be addressed by evaluating genotypes between environments, development of selection goals and multitrait selection. Improving artificial insemination, ram breeding capacity, obtaining puberty and quantifying embryonic loss will be addressed across a background of varying breeds and nutrition levels. Changes in body composition and mechanisms controlling forage intake will ultimately lead to a better understanding and approach for supplementation strategies. Growth and body composition data will be developed and utilized to evaluate sheep growth and the relationships between mature size and body composition. This information will be extended to an extent sheep simulation model which will have the long term goal of being used as a basis for a decision support system.

NATIONAL ANIMAL GERMPLASM PROGRAM

Project: 5402-31000-001-00D

Location: Fort Collins, Colorado

Researchers: H. Blackburn

Objectives:

(1) Development and coordination of the National Animal Germplasm Program, including database development, data collection, entry and curation, coordination of germplasm inventory, plan and conduct meetings with stakeholders, conduct research to enhance animal germplasm preservation, and disseminate information about the program and specific information about the preserved germplasm available for each species.

Approach:

Develop an animal germplasm database by adding an animal component of the GRIN (Genetic Resources Information Network) database in cooperation with the GRIN database manager. Information about cryopreserved or in-situ preserved germplasm at ARS and non-ARS locations will be collected, entered into the GRIN database, and curated. Germplasm stored at the National Seed Storage Laboratory will be inventoried, monitored and distributed according to species committee's recommendations. Plan and conduct stakeholder meetings, augment and interact with animal germplasm preservation efforts by other groups, and disseminate information about the program and germplasm in storage by the world wide web and other medias. Conduct research to enhance preservation of germplasm.

IMPROVING SEEDSTOCK SELECTION DECISIONS TO FACILITATE COST-EFFECTIVE PRODUCTION OF HIGH QUAL. BEEF

Project: 5434-31000-009-00D

Location: Miles City, Montana

Researchers: M. MacNeil
E. Grings
R. Bellows
R. Heitschmidt
R. Short
M. Haferkamp
M. Grosz

Objectives:

(1) Define genetic merit from component traits that may be antagonistically correlated.

(2) Identify molecular genetic markers associated with traits of economic and/or biological importance.

(3) Develop genetic evaluation systems that accurately predict merit from available quantitative and molecular information.

(4) Validate efficacy of new knowledge and technology in accelerating genetic improvement.

Approach:

Continue selection to improve biological efficiency of beef production based on increased values of the index: yearling weight minus birth weight multiplied by 3.2 or calf weight at weaning divided by cow weight. Monitor environmental trend using a randomly mated and randomly selected control. Measure correlated responses to selection in growth, food intake, reproduction, and carcass attributes. Develop backcross resource families for identifying molecular genetic markers segregating between Line 1 Hereford and CGC composite populations. Associate molecular markers with phenotypic components of biological and economic importance. Conserve unique Line 1 Hereford germplasm and continue historic practice of selecting for increased postweaning growth. Statistically integrate biological and economic information to develop technology to consistently select beef cattle whose offspring are more profitable or efficient and produce products that meet consumer expectations.

OPTIMIZING REPRODUCTION EFFICIENCY TO ENHANCE PROFIT & SUSTAINABILITY OF RANGE BEEF PRODUCTION

Project: 5434-31000-010-00D

Location: Miles City, Montana

Researchers: R. Bellows
R. Heitschmidt
E. Grings
R. Short
M. Haferkamp
M. MacNeil
M. Grosz

Objectives:

Optimize reproductive efficiency by:

(1) Identifying physiological, endocrine and molecular mechanisms controlling calf development and survival from conception to weaning; ascertaining genetic, nutritional, and physiological factors controlling pregnancy and the transition from the anestrual to estrual state; manipulating reproductive, genetic and nutritional interactions to enhance profitability and sustainability of range beef production.

Approach:

Varying diets will be fed in dry lots or on range to determine maternal & fetal differences in metabolites, hormones, fetal growth, dystocia, calf survival from birth to weaning, & reproduction of the dam. Response of the neonate to low temperatures will be determined in controlled temperature environments. Perinatal physiology of dam & fetus will be determined by blood samples and radio telemetric monitoring & related to calf survival & reproduction of the dam. QTLs that improve reproduction will be identified. Action mode cause-&-effect relationships in pine needle-induced abortion will be determined. Prepuberal & postpartum females will be fed varying diets & effects on transition from the anestrual to estrual state determined. Novel methods for induction or synchronization of estrus in beef females will be developed & evaluated. Animals of varying genotypes on supplements including annual & perennial forages during the annual reproduction cycles will be used to determine effects of management systems on productivity, production costs & sustainability of natural resources.

NUTRITIONAL AND MANAGEMENT STRATEGIES TO IMPROVE REPRODUCTIVE PERFORMANCE IN GILTS AND SOWS

Project: 5438-31000-040-00D

Location: Clay Center, Nebraska

Researchers: J. Klindt
J. T. Yen

Objectives:

Develop nutrition and management strategies to ensure:

(1) Gilts express puberty and conceive in a concise and timely manner.

(2) Sows mate and conceive within a timely interval after weaning.

Approch:

Nutritional environment, has short- and long-term effects on physiological development. A series of studies will be conducted to test the following hypotheses concerning the role of nutritional environment in determining reproductivity of gilts and sows: 1) Faster growing females cycle and conceive more readily than those gaining slower. 2) Dynamic measures of gain in females are more indicative of reproductivity than static measures of composition. 3) Faster gaining animals have patterns of hormone secretion and clearance different than slower gaining animals. 4) Faster gaining animals have higher rates of metabolism than those gaining slower. 5) Limit-fed developing animals acquire greater ability to mobilize and replenish tissue stores. 6) Inadequate bioavailability of metal-amino acid complexes to hypothalamus limit reproductivity of sows. Studies will use differing levels of nutrition, serial slaughter, calorimetry, measures of hormone and metabolite levels and clearance to identify effects of nutritional environment on reproductive efficiency.

IDENTIFY QUANTITATIVE TRAIT LOCI AFFECTING OVULATION IN CATTLE

Project: 5438-31000-041-00D

Location: Clay Center, Nebraska

Researchers:

Objectives:

(1) Identify Quantitative Trait Loci (QTL) affecting ovulation in cattle.

(2) Evaluate effects of QTL and implement Marker Assisted Selection.

(3) Develop additional markers from chromosome specific libraries to fine map QTL.

(4) Identify genes that regulate ovulation and determine their role in follicular dynamics.

Approach:

Tissue samples and semen have been collected from a population selected for two ovulations. A number of evenly spaced markers (~10cM) covering the entire genome will be genotyped across a subset of the animals to screen for QTL affecting ovulation. Additional animals and markers will be used to map the QTL to smaller intervals. Markers that are closely linked to the QTL will be used to validate the QTL's level of effect upon ovulation in the model population and other unselected populations. Additional markers will be generated in regions containing QTL for fine mapping and Marker Assisted Selection. Utilizing our bovine YAC library, genes regulating critical components of ovulation will be identified and sequenced. The role of these genes in regulating follicular growth, ovulation and fertilization will be investigated in different populations.

DEVELOPMENT OF AN EFFICIENT SYSTEM FOR PRODUCTION OF MEAT-TYPE PIGS IN THE SOUTHERN UNITED STATES

Project: 5438-31000-042-00D

Location: Clay Center, Nebraska

Researchers: R. Christenson

Objectives:

(1) Evaluate four (4) breeding lines for prolificacy and carcass characteristics.

(2) Develop feeding systems to obtain efficient biological conversion and minimize feed cost by using local feeds such as rice by-products as appropriate.

Approach:

Initially, a physical facility will be developed and an effective breeding and production program will be implemented to provide a basis for conducting swine production research. Lines of swine will be selected to establish maternal and paternal lines that can perform under the environmental conditions in the southern United States. A production program will be developed to ensure appropriate levels of fertility and litter size. Nutritional diets for swine at all stages of the life cycle that lead to optimum feed efficiency and rate of growth at lowest cost, utilizing local feeds whenever possible, will be established.

IDENTIFY MARKERS TO ENHANCE GAMETE PRODUCTION IN SWINE

Project: 5438-31000-045-00D

Location: Clay Center, Nebraska

Researchers: J. Ford
T. Wise

Objectives:

(1) Identify genomic markers and endocrine regulators of ovulation in sows.

(2) Identify genomic markers and endocrine regulators of sperm production in boars.

(3) Develop greater understanding of regulation of ovarian follicular development and design management protocols that utilize these findings.

Approach:

Major reproductive constraints that restrict efficiency of swine enterprises include delayed puberty, slow return to estrus after weaning and required maintenance of a high number of breeding boars. All three of these result from incomplete understanding of regulation of gamete production. For the proposed studies, genetic lines of swine that have distinct differences in gamete production will be used. Gonads and pituitary glands of boars and gilts will be evaluated during pubertal development to identify biochemical, genomic and histological traits that correlate with subsequent differences in ova and sperm production. Genetic markers will be identified by using an existing swine genomic map and measuring variation for gamete production in specific reference populations. Management programs will be evaluated for their potential to hasten estrus and ovulation in prepubertal gilts and weaned sows. Particular emphasis will be placed on synthesis and secretion of follicle stimulating hormone.

GERMPLASM EVALUATION AND IMPROVED REPRODUCTIVE FUNCTION IN THE BULL, BOAR AND RAM

Project: 5438-31000-044-00D

Location: Clay Center, Nebraska

Researchers: D. Lunstra

Objectives:

(1) Characterize breed differences for testis development and semen quality in bulls representing unique germplasm for potential improvement of existing U.S. breeds for beef production.

(2) Identify genomic markers and biological regulators for increased reproductive efficiency in bulls,boars, and rams.

(3) Develop procedures to identify young sires (bulls, boars, and rams) of superior fertility.

Approach:

Accurate procedures to predict the reproductive potential and fertility of young herd sires are lacking for all three major meat animal species. In addition, new breeds/germ plasm frequently are being imported to provide improved lean growth rate, disease resistance, heat tolerance, etc., but often little is known about their reproductive characteristics. This research will characterize breeds for differences in age at puberty, testicular development, testis structure, efficiency of spermatogenesis and semen quality, and breeds/individuals that differ dramatically in these factors will be studied to identify the genomic markers and biological regulators involved. In cattle, these factors will be characterized in bulls of Africander, Mashina, Romo Sinuanu, Senepol, Swedish Friesian and Wagyu breeds and compared to data from Angus and Hereford bulls. In swine, regulatory factors that allow the Chinese Meishan boar to achieve much earlier puberty and higher efficiency of sperm production than do typical U.S. breeds of boars will be identified and evaluated.

GENETIC AND PHENOTYPIC DETERMINANTS OF LITTER SIZE IN SWINE

Project: 5438-31000-043-00D

Location: Clay Center, Nebraska

Researchers: R. Christenson
H. Klemcke
J. Vallet

Objectives:

(1) Identify genomic markers for breeding performance and uterine capacity in swine.

(2) Identify maternal, uterine, and conceptus phenotypic factors that determine uterine capacity and litter size in swine.

(3) Identify genetic and management practices to improve breeding performance and litter size in gilts and sows.

Approach:

Breeding performance (age of puberty, anestrus, conception rate) and litter size of gilts and sows have been identified as economically important reproductive traits. Litter size is primarily limited by uterine capacity. Genomic markers for breeding performance and uterine capacity will be identified by measuring their phenotypic variation in current swine genomic reference populations. Gene mapping techniques will be used to associate phenotypic variation with specific areas of the swine genome. Physical traits (e.g., placental size, ovarian weight, uterine length) and biochemical mechanisms (e.g., conceptus elongation, uterine protein secretion, fetal liver function, fetal blood cell formation) associated with uterine capacity will be identified. Meishan pigs, lines selected for uterine capacity, and the unilateral hysterectomized-ovariectomized swine model will be used in these investigations. Identified physical traits and biochemical mechanisms will be used for genetic selection, gene mapping,and management programs to improve reproductive efficiency of swine.

IMPROVING GENETIC PREDICTION OF ECONOMIC MERIT OF DAIRY ANIMALS

Project: 1265-31000-069-00D

Location: Beltsville, Maryland

Researchers: H. D. Norman
CU. Van Tassell
P. Raden
R. Norman
G. Wiggans

Objectives:

(1) Maintain national database for genetic research on milk yield, composition and fitness traits.

(2) Develop improved methods for comparing genetic evaluations across countries.

(3) Investigate accuracy of alternative methods of genetic evaluation.

(4) Determine ecomonic values of health and reproductive traits and develop measures of overall merit that included these traits.

(5) Determine feasibility of using genetic markers to improve the accuracy of evaluated traits and prediction efficiency.

Approach:

Expand the national database for dairy records by storing test-day instead of lactation data; provide more timely editing of records through daily submissions to the database; determine possible biases in current International Bull Evaluation Service procedures by investigating ability of international evaluations to predict future national evaluations; increase accuracy of evaluations by using multitrait analysis; compare results from a test-day model with those from the current lactation model to determine if it improves prediction of future progeny performance; evaluate current fertility data to determine their value in selection programs; improve economic indexes by estimating the relationships among traits and by updating relative economic values after literature review; develop a test-day model for traits such as productive life and somatic cell score; create a new semem repository for use in verification of quantitative trait loci (QTL) and estimation of allelic affects; develop tools to describe identified QTL based on experiment-wise error rates.

SEX PRESELECTION IN MAMMALS AND SPERM PRESERVATION IN LIVESTOCK AND POULTRY

Project: 1265-31000-060-00D

Location: Beltsville, Maryland

Researchers: L. Johnson
A. Donoghue

Objectives:

(1) Improve methods to evaluate sperm which correlate with fertilization.

(2) Develop new sperm viability tests for turkey sperm; develop methods for short-term (24-48 hr) storage of turkey sperm in vitro; study in vitro mechanisms of sperm storage.

(3) Evaluate fundamental cryobiological factors that impact sperm survivial.

(4) Elucidate fluorescent stain effects on sperm and embryos following cell sorting of mammalian spermatozoa.

(5) Optimize sexing technology with in vitro fertilization & sperm preservation protocols.

Approach:

Use flurogenic stains in combination with flow cytometry to assess various properties/functional characteristics of individual sperm that may be related to potential fertilizing capacity. Use oviductal in vitro culture to evaluate metabolic, ionic and physical components important to sperm function in vivo. Use a combination of cryomicroscopy, supravital stains and flow cytometric analysis to evaluate effects of freeze-thaw procedures on sperm membrane integrity and overall sperm survival. Determine toxicity factors that may be associated with sorted sperm as related to presence of fluorescent stains and evaluate effects of developing embryos using fluorescent probes. Use sorted sperm to fertilize eggs in vitro to determine fertilizing capacity.

USDA ANIMAL HORMONE PROGRAM & THE FUNCTION OF GENES REGULATING TURKEY EGG PRODUCTION & EMBRYOGENESIS

Project: 1265-31000-065-00D

Location: Beltsville, Maryland

Researchers: J. Proudman
M.. Bakst

Objectives:

(1) Determine the role of the prolactin receptor in regulating egg production in the turkey hen.

(2) Identify key genes which regulate egg laying.

(3) Search for polymorphisms in reproductive genes.

(4) Describe the biological basis of embryo mortality during development.

(5) Describe the sequence of cellular and molecular events attending fertilization, activation of development, and embryogenesis.

(6) Provide research reagents through the USDA Animal Hormone Program, and develop new reagents essential for farm animal research.

Approach:

Measure prolactin (PRL) Receptor gene expression to determine target tissues for PRL action and correlate gene expression with reproductive performance. Identify endocrine and paracrine factors which initiate incubation behavior by studying changes in lactotrophs during onset of incubation behavior using immunohistochemistry and in situ hybridization. Polymorphisms in genes which regulate reproduction will be identified by RFLP analysis. Chicken thyroid stimulating hormone will be purified and an homologous radioimmunoassay will be developed. Determine relative rate of blastodermal cell apoptosis and necrosis within each stage of embryo development (to 72 hr of incubation) in fresh and stored (30 days) eggs. Determine mechanism of temperature induced suppression of embryo development and impact of prolonged egg storage on activation of embryogenesis at the onset of incubation. Characterize stage specific development using gene markers, cell lineage studies, and manipulation of blastoderm explant.

OOCYTE AND EMBRYO DEVELOPMENT, CONSERVATION, AND PRESERVATION IN SWINE

Project: 1265-31000-070-00D

Location: Beltsville, Maryland

Researchers: H. Guthrie
J. Dobrinsky

Objectives:

(1) Produce new knowledge of specific genes in the oocyte and follicular environment that can be manipulated to improve the efficiency of the oogenesis, follicular growth, resumption of meiosis, fertilization and embryonic developmental competence.

(2) Determine how embryonic gene function and structure are affected by factors in the culture environment and by cryopreservation techniques in order to improve subsequent embryo and fetal survival in surrogate females.

Approach:

Gene expression, metabolic activity, and cell structure important to specific areas of research in oocyte and embryo development will be determined by using immunohistological techniques, confocal microscopy, DNA fluorescence flow cytometry, in situ hybridization, and semi-quantitative reverse transcriptase polymerase chain reaction. The role of specific genes, ovarian innervation, cell proliferation, and apoptosis in the growth and maturation of oocytes and antral follicles will be elucidated. Aspects of the follicle environment that regulate oocyte developmental competence will be determined by in vitro maturation/fertilization of individual oocytes and by in vivo fertilization of transferred oocytes matured in vitro and in vivo. The genetic, metabolic, and structural characteristics of embryos required for successful development in vitro and for subsequent survival in surrogate females, will be investigated in relation to different culture and cryopreservation techniques.

IDENTIFICATION AND MAPPING OF GENES INVOLVED IN PARASITIC DISEASE RESISTANCE/SUSCEPTIBILITY

Project: 1265-31320-012-00D

Location: Beltsville, Maryland

Researchers: J. Lunney
L. Gasbarre
H. Lillehoj

Objectives:

(1) Identify and breed livestock and poultry that are genetically resistant to parasite infections.

(2) Define response phenotypes of parasite resistant vs susceptible animals.

(3) Assess role of candidate genes in encoding parasitic disease resistance/susceptibility.

(4) Use flow sorted and microdissected chromosomes to develop new swine chromosome specific genetic markers.

(5) Use species genome maps to begin to correlate genotype markers with phenotypic traits associated with parasitic disease resistance/susceptibility.

Approach:

Identification of the genes that regulate parasite resistance/susceptibility of livestock and poultry will be carried out by evaluating genetic variations in host responses to challenge infections with defined parasite inocula in genetically defined populations; identifying resistant versus susceptible populations by comparative correlation of post infection parasite burdens with protective immunological responses between the different genetic groups; assessing the role of candidate genes by correlating genotypes with parasite resistance and identifying phenotypic traits associated with various immunological responses; developing new chromosome specific microsatellite markers for detailed genome mapping in pigs; mapping the alleles of genes that closely correlate with a specific disease phenotype in swine, cattle and chickens to correlate genotypic markers with phenotypic traits associated with parasite disease resistance/susceptibility.

CATTLE MUCOSAL IMMUNITY AND RESPONSES TO PARASITIC INFECTIONS

Project: 1265-32000-054-00D

Location: Beltsville, Maryland

Researchers: L. Gasbarre
M. Jenkins
D. Zarlenga

Objectives:

(1) Assess cattle mucosal immunity & responses to parasitic infections.

Specific Objectives

(1) Expand understanding of immune responses to parasites of cattle including Neospora, Coccidia, nematodes, emphasizing mucosal immune responses & cytokines & antigens regulating these responses.

(2) Utilize host immunity to control these infections.

(3) Develop molecular methods to identify parasite species; clone & express individual parasite genes.

(4) Apply research to working production systems reducing parasite-induced loss.

Approach:

Immune respones of cattle experimentally or naturally infected by parasites that reside in or invade the host via mucous membranes will be defined. Studies will focus on gastrointestinal nematodes and protozoa (Neospora, Eimeria),but will be adaptable to many cattle mucosal parasites. Studies define lymphocyte populations and cytokine induction patterns in cattle susceptible or immune to infection by the parasites. Once protective immune responses are identified, methods to enhance or dampen ineffective responses will be investigated. Parasite components or products that stimulate/suppress the host immunity will be identified, characterized and cloned for studies of gene regulation, and for the production of recombinant forms for in vivo use. New molecular and/or immunologic diagnostic tools will be evaluated for their ability to discern exposure to the parasites, or for characterization of the disease state. Real-world production systems studies will evaluate the effectiveness of the parasite control programs.

GENETIC MAPPING OF QUANTITATIVE TRAIT LOCI IN DAIRY CATTLE

Project: 1265-31000-061-00D

Location: Beltsville, Maryland

Researchers: M. Ashwell
K. Maruyama
T. Sonstegard
C. Van Tassell

Objectives:

(1) Genetically map quantitative trait loci (QTL) affecting health and production traits in dairy cattle.

(2) Genetically map butyrophilin gene in dairy cattle and determine if the gene is associated with health and milk production QTL.

(3) Construct and screen cDNA libraries from reproductive tissues of cows to identify genes which are involved in the maintenance of pregnancy.

Approach:

Microsatellite markers (ms) will be used to genotyped US Holstein families to identify health and milk production QTL. Three ms from each chromosome (chr) will be genotyped in 7 families. Selective genotyping and the grand daughter design will be used to reduce the number of genotypings needed. Analysis will identify possible associations between specific chr regions and the studied traits. Markers showing significant associations will be further studied by genotyping additional sons from informative families to determine an unbiased estimate of the effect. Mapping of the butyrophilin gene (but) will be accomplished by identifying a PCR-RFLP associated with the gene and flanking ms will be used to determine if but is associated with any health or milk production QTL. Reproductive tracts and embryos will be collected from pregnant and nonpregnant cows at critical stages and cDNA libraries will be constructed from these tissues. Clones will be sequenced to identify genes which are unique to pregnancy at different stages.

MOLECULAR AND CELLULAR STRATEGIES TO ENHANCE THE GERMPLASM AND GENOME OF LIVESTOCK

Project: 1265-31000-066-00D

Location: Belltsville, Maryland

Researchers: V. Pursel
N. Talbot
K. Wells

Objectives:

(1) To determine the potential of transferring cloned genes into the genomes of farm animals to improve their growth performance, to enhance the quality of their meat and milk, or to increase their resistance to disease.

(2) Develop methods to derive stem cell lines that can be genetically modified and contribute to the germ line of livestock.

Approach:

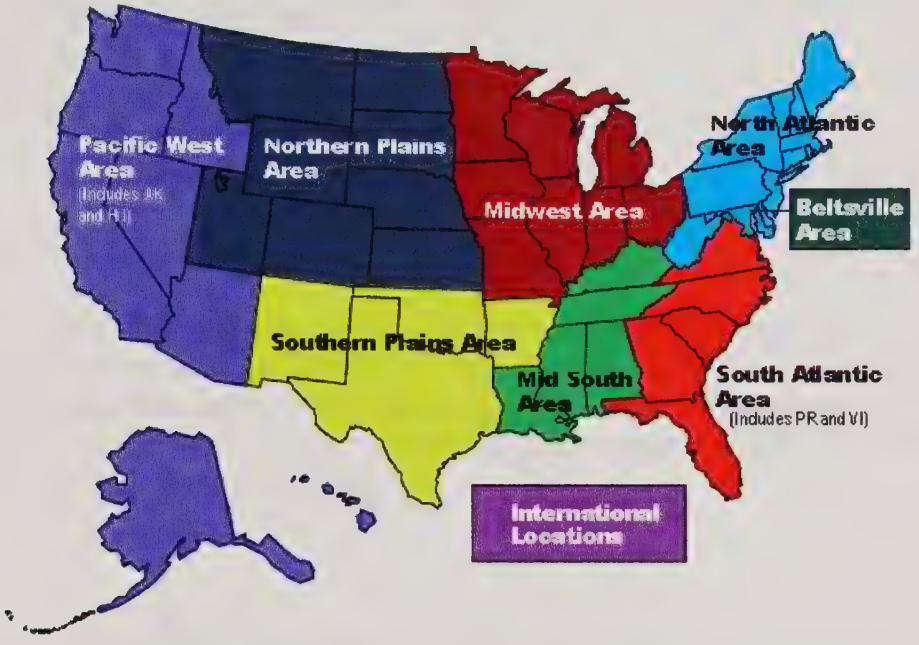
Fusion genes will be microinjected into pronuclei of zygotes & transferred into surrogate females to develop. At birth, tail tissue will be evaluated for presence of the transgene. Expression of the transgene will be determined by assaying blood, muscle, or milk as appropriate for the gene product by radioimmunoassay, northern blot, or western blot analysis. Transgenic founders & their progeny will be evaluated for phenotypic affects on growth rate, carcass composition, milk composition, or disease resistance as appropriate for the specific transgene. Growth factor will be screened for the ability to maintain undifferentiated morphology of cell lines cloned from embryos. Blastomeres from 4 to 16-cell embryos will be co-cultured to determine their abilty to produce pluripotent cell lines. Lines will be characterized for their expression of a number of genes that reflect their state of differentiation.

ARS National Program 102

Research Areas and Project Locations

ARS Research Locations

for the National Program for Animal Production Systems



Beltsville Area	Livestock and Poultry Sciences Institute, Beltsville, MD (http://www.lpsi.barc.usda.gov/)
Midwest Area	U.S Dairy Forage Research Laboratory, Madison, WI (http://www.dfrc.ars.usda.gov/) Soil and Water Management Research Unit, St. Paul, MN (http://www.)
North Atlantic Area	Plant Soil and Nutrition Laboratory, Ithaca, NY (http://www.arserrc.gov/naa/home/fedpsnl.htm)
Northern Plains Area	Fort Keogh Livestock and Range Research Laboratory, Miles City, MT (http://www.npa.ars.usda.gov/_private/NPA/noplains.htm) Roman L. Hruska U.S. Meat Animal Research Center. Clay Center, NE (http://www.marc.usda.gov/)
Pacific West Area	U.S. Sheep Experiment Station, Dubois, ID (http://pwa.ars.usda.gov/usses/)
South Atlantic Area	Subtropical Agricultural Research Station, Brooksville, FL (http://www.ifas.ufl.edu/~starsweb/)
Southern Plains Area	Dale Bumpers Small Farm Research Center, Booneville, AR (http://www.booneville.ars.usda.gov/) GrazinglandsResearch Laboratory, El Reno, OK (http://grl.ars.usda.gov/)

CONTROL OF APPETITE IN POULTRY, BEEF, AND SWINE

Project: 1265-31000-068-00D

Location: Beltsville, Maryland

Researchers: J. McMurtry
T. Caperna
M. Richards

Objectives:

(1) This research will examine at a whole animal, tissue and gene level appetite control mechanisms of poultry and swine by determining the effects of food intake on key regulatory gene expression elements and peptide synthesis, including neurotransmitters. Using genetic variants currently available, partition voluntary appetite regulation into that attributable to peripheral and CNS control elements.

Approach:

Research will focus on developing species-specific techniques to quantify leptin gene expression and tissue and blood levels of leptin. cDNA libraries will be screened for chicken and pig leptin. Native leptin and/or a fragement peptide will be produced by recombinant technology. Leptin-brain neurotransmitter interactions will be investigated as it relates to feed intake. Exogenous compounds such as growth hormone which impact appetite will be administered to investigate brain neuropeptide turnover. Different genetic models, such as the red jungle fowl and the obese pig, will be utilized to determine whether differences in leptin gene expression that exist can account for inherent differences in feed intake.

GENES ENHANCING/LIMITING LEAN TISSUE ACCRETION

Project: 1265-31000-071-00D

Location: Beltsville, Maryland

Researchers: A. Mitchell
T. Caperna
T. Ramsay

Objectives:

Information is needed to ascertain which genes are positively impacting growth in broiler chickens versus those that may have negative effects. We will identify genes involved in steps that regulate lean/fat tissue accretion, determine the feasibility of gene manipulation in improving the efficiency of lean tissue synthesis and use new methods of indirect measurements to determine the effects of gene manipulation on body composition.

Approach:

This research project seeks to investigate the molecular basis for fat metabolism in poultry and muscle metabolism in swine to maximize the probabilities for success. The primary purpose will be to determine specific genes that respond to either permutations in diet, dietary regimens or hormone treatments. To identify these genes we propose to use several animal models which have very different background growth characteristics. Genes expressed at different levels will be determined using RTP-PCR and Northern analysis to confirm the expression pattern. Another purpose will be to determine if genes can be modified with certain specific dietary ingredients (nutriceuticals) or hormone treatments (thyroid hormones). Genes whose activities parallel relatively simple manipulations will be outlined. This objective will be centered on planned modifications of the expression of the UCP2 & 3 genes. Lastly the feasibility of gene manipulation in improving the efficiency of lean tissue synthesis will be assessed by using DEXA.

ENDOCRINE AND IMMUNE MECHANISMS AFFECTING GROWTH IN YOUNG CATTLE

Project: 1265-31320-013-00D

Location: Beltsville, Maryland

Researchers: T. Elsasser
T. Rumsey
T. Ramsay

Objectives:

Improve growth in young beef cattle by 1) setting nutritional and physiological criteria for a responsive and sensitive model for protein accretion through use of growth promoters, and nutrients (including protein, energy, fatty acids and amino acids), and 2) Define the metabolic cost in terms of calories and reduced protein accretion for animals challenged with physiological models that reduce growth, and determine the efficacy of hormonal treatments to prevent this reduced growth.

Approach:

Three growth/slaughter balance trials of up to 30 animals each will be used to 1) define and establish dietary energy and protein levels for young cattle that allow exogenous growth hormone to channel more nutrients into carcass and muscle protein, rather that gut and visceral tissue, and 2) determine the effects of specific fatty acids and (or) amino acids on growth, body composition, and endocrine and immune status in young growing cattle with particular emphasis on growth mechanisms underlying changes in physiological status. Three immune system challenge studies of up to 40 animals each will be used to 1) compare the ability of various steroid-based growth promoters and specific dietary nutrients to enhance resilience of cattle to overcome physiological stresses, and 2) define changes in somatotropic axis (GH and IGF-I) and immune cytokine (tumor necrosis factor-a and nitric oxide) signal transduction mechanisms that mediate changes in metabolism and down regulation of growth accompanying tissue wasting during parasitism and endotoxemia.

NUTRITIONAL AND PHYSIOLOGICAL FACTORS AFFECTING SPLANCHNIC ENERGY METABOLISM IN RUMINANTS

Project: 1265-31000-063-00D

Location: Beltsville, Maryland

Researchers: R. Baldwin
K. McLeod
F. Byers
A. Lefcourt

Objectives:

(1) The objective of this project is to elucidate the mechanism(s) by which increased feed energy intake augments oxidative metabolism by the splanchnic tissues of ruminants. This will be accomplished through the integration of in vitro assessments of gut tissue metabolism with measurements of net nutrient metabolism by splanchnic tissues and measurements of whole body energy metabolism obtained using indirect calorimetry.

Approach:

To establish factors involved in the response of splanchnic tissues to increased energy intake, and ultimately the mechanism regulating the response, an integrated approach with measurements of energy metabolism made at the whole animal, tissue bed and tissue and cellular levels will be used. Three specific experimental approaches will be used to assess the response in growing sheep and steers: 1) effects of energy density and level of intake, 2) effects of specific dietary energy components and site of delivery, and 3) extent to which energy alone mimics the effects of increased energy density and increased energy intake. Determinations will include whole animal responses using indirect-respiration calorimetry, in vivo net flux of hormones and nutrients across splanchnic tissues, and tissue metabolism in vitro, rates of protein synthesis, cell proliferation, and synthesis of specific growth factors and corresponding receptors.

IMPROVING RUMINAL FERMENTATION

Project: 1907-31000-003-00D

Location: Ithaca, New York

Researchers: J. Russell
L. Kochian

Objectives:

(1) Genetically modify the ruminal bacterium Bacteroides ruminicola, so that it will be able to digest cellulose at low pH.

(2) Define more completely the mechanism of energy spilling in ruminal bacteria.

(3) Modify on the Cornell Net Carbohydrate-Protein System so it can accomodate the feed additive monensin.

Approach:

The carboxymethylcellulase gene of PREVOTELLA RUMINICOLA will be modified to include a cellulose binding domain and a P. RUMINICOLA promoter, and the modified gene will be returned to P. RUMINICOLA in an attempt to create an acid-resistant cellulolytic bacterium. The energy spilling reaction of STREPTOCOCCUS BOVIS will be studied to determine if fructose 1,6 diphosphate is an allosteric regulator of the membrane bound ATPase. The Cornell Net Carbohydrate Protein System will be modified to include an additional pool of obligate amino acid fermenting bacteria and an accommodation for nitrogen deprivation and energy spilling reactions.

REDUCTION OF SWINE PRODUCTION ODOR THROUGH NUTRITION AND MICROBIOLOGY

Project: 3625-31000-001-00D

Location: Ames, Iowa

Researchers: J. Hatfield
J. Crouse

Objectives:

(1) Determine the effect of alternative diet formulations on excretion of odor while optimizing performance.

(2) Localize (map), characterize, and alter the in situ microflora of the pig gut to reduce odor production and improve nutritent utilization.

(3) Determine the role of the endogenous pig gut on the population of microbes that reside within the gut.

Approach:

Determine the effects of alternative diet formulations within various swine production stages, that incorporate nontraditional feedstuffs, and methods of feed preparation, on excretion of odor and nutrients while optimizing reproduction, growth, and development. Localize and characterize the complete in situ microflora populations in various sections of the pig gut and determine factors such as feed, components, developmental stages of the pig, and phases of production which influence the makeup of these populations. Determine the specific microbes and their metabolic pathways in generating odor and inhibiting nutrient utilization by the pig and thereby develop methods of modified microflora. Determine if endogenous "signals" in the pig gut, such as peptides, acids, bases, vitamins, etc., influence the microbes which reside there and isolate the host genes that regulate these "signals".

IMPROVING FORAGE FIBER DIGESTIBILITY

Project: 3640-31000-003-00D

Location: St. Paul, Minnesota

Researchers: H. Jung

Objectives:

Increasing energy availability to dairy cows from forage crops by improving fiber digestibility through genetic selection, reducing lignin/polysaccharide cross-linking, and increasing accessibility of tissues to digestion.

Approach:

Inbred and hybrid corn lines will be evaluated for fiber digestibility of the stover portion of silage. Experimental hybrids will be created to determine the heritability of fiber digestibility in corn silage. Alfalfa will be selected for improved stem fiber digestibility and cell-wall composition. The impact of lignin/polysaccharide cross-linkage on fiber digestibility will be assessed in a mutant corn line with reduced concentrations of ferulate esters, the precursor of cross-link formation, and smooth bromegrass plants selected for divergent levels of cross-linking. The gene(s) controlling ferulate ester deposition in cell walls will be isolated from the mutant corn line. Limits to degradation of forage stem tissues due to accessibility constraints imposed by cellular structure will be compared to traditional measures of chemical composition. Rumen fiber degrading bacterial species will be characterized for their ability to degrade specific tissues and cell-wall polysaccharides.

CELL WALL FACTORS LIMITING DIGESTIBILITY AND FORAGE UTILIZATION IN SUSTAINABLE DAIRY FARMING

Project: 3655-21000-028-00D

Location: Madison, Wisconsin

Researchers: J. Ralph
R. Hatfield
P. Weimer
D. Mertens
R. Smith
J. Grabber
N. Martin

Objectives:

(1) Characterize plants with genetically modified lignification to develop novel approaches for improving forage utilization.

(2) Determine the extrinsic role of rumen environment upon forage digestion, fermentation efficiency, and formulation of indigestible residues.

(3) Determine chemical characteristics of indigestible residues to elucidate the mechanism(s).

(4) Develop and test strategies that include genetic selection to improve cell wall degradation.

Approach:

A diverse set of plants, both natural mutants and molecularly altered plants, containing mutations affecting major steps of the lignin monomer pathway will be characterized in order to develop novel approaches for improving forage utilization and provide insight into the complex effects of lignin composition on cell wall digestibility and the consequent formation of indigestible residues. Rumen environmental factors, such as pH, specific microbial populations, and their dynamic interactions will be evaluated to determine effects on the digestion kinetics of cell wall components in vitro and in vivo. A range of forages reflecting differences in plant tissues and maturity will be degraded using rumen microbes to generate indigestible residues for chemical & structural characterization. Forage legume germplasm will be evaluated for desirable cell wall composition (e.g., pectin) to help guide genetic selection programs to improve digestibility.

IMPROVING THE SUSTAINABILITY OF DAIRY FARMS BY USING SITE-SPECIFIC ESTIMATES OF NUTRITIVE VALUE

Project: 3655-31000-015-00D

Location: Madison, Wisconsin

Researchers: D. Mertens
R. Muck
J. Grabber
G. Broderick
N. Martin

Objectives:

(1) Identify critical parameters that affect the nutritive value of feeds including feed characteristics, crop genetics, growing conditions, harvesting, storage, processing, ration, and animal type.

(2) Quantify factor affecting nutritive value.

(3) Develop an expert system that integrates information about laboratory analyses; crop growing, harvesting, and storage conditions; and animal/ration characteristics to provide site-specific estimates of energy availability and digestion kinetics.

Approach:

An expert system will be designed to gather information from users, estimate critical missing information, match input information with that in a feed information database, and integrate all available information to provide site-specific estimates of a feed's nutritive value. The expert system will be programmed in C++ using a variety of techniques including regression, neutral networks, and simulation models. The information to build these relationships and models will be taken from previously collected research data and, where necessary, new laboratory, greenhouse, field, and animal studies. A key component is the feed information database. The database will be developed to provide internally consistent information about the description, chemical composition, physical properties, and bioavailabilities of feeds. The database will be compiled initially from published sources. Later, representative feeds will be analyzed using the same analytical system with adequate quality control to develop an internally consistent and well-documented database.

IMPROVING EFFICIENCY OF NITROGEN UTILIZATION IN DAIRY PRODUCTION

Project: 3655-31000-016-00D

Location: Madison, Wisconsin

Researchers: G. Broderick
R. Hatfield
R. Muck
R. Koegel
L. Satter
R. Smith
N. Martin

Objectives:

(1) Milk is one of the best sources of high quality protein in American diets; however, inefficient utilization of dietary N by dairy cows increases cost, increases milk price, and increases pollution. Improving protein efficiency in dairy cows will be addressed by developing: methods to reduce protein breakdown to nonprotein N in silages; rapid and accurate methods for quantifying ruminal protein degradation; and practical strategies for optimizing ruminal balance between protein degradation and synthesis.

Approach:

Techniques will be developed for reducing silage NPN. Red clover yields silage with lower NPN than alfalfa; the reduced NPN results from the action of polyphenol oxidase (PPO). Research will characterize the red clover PPO, evaluate results from isolation and transfer to the PPO gene to alfalfa, and enhance PPO activity of red clover germplasm using recurrent phenotypic selection. Other work will evaluate modified atmospheres and mechanical conditioning for decreasing silage NPN. Methods will be developed for rapid and precise measurement of ruminal protein degradation. The inhibitor in vitro system will be used to validate methods based on proteases and near infrared reflectance. Strategies will be developed for improving protein utilization through synchronizing protein synthesis and degradation in the cow's rumen. Research will evaluate unique corn silage hybrids and new processing methods for increasing ruminal protein formation in vivo and enhancing utilization of degraded protein. Other research will evaluate the Cornell System and other widely applied feeding models.

RANGELAND ECOLOGY, MANAGEMENT AND UTILIZATION BY SHEEP

Project: 5364-31610-001-00D

Location: Dubois, Idaho

Researchers: J. Hendrickson
H. Blackburn

Objectives:

(1) Develop and evaluate methods for monitoring and determining the health of rangeland ecosystems.

(2) Determine how sheep can be used as a biological tool for plant manipulation e.g. noxious weeds.

(3) Quantify winter forage dynamics and nutrient requirements of ewes for development of cost effective supplementation strategies.

Approach:

Quantification of plant species and plant community dynamics on sagebrush steppe and sub-alpine ranges will be evaluated. Vegetation will be sampled during growing seasons. Research on sagebrush steppe will be coordinated with the ARS carbon sequestration network. Plant species data will feed up into an analysis of plant community dynamics with and without grazing. An evaluation of extant range simulation models will be performed to determine their accuracy for the ranges evaluated. Studies addressing the interaction between diet selection on winter range will be performed to establish nutrient balance of pregnant ewes so as to develop cost effective supplementation strategies. Control of noxious weeds by sheep will be evaluated by a series of factorial experiments involving the time of grazing, the duration of grazing and grazing in combination with herbicide use. REPLACED part of 5364-31630-003-00D.

LOW RISK MANAGEMENT STRATEGIES FOR SUSTAINING RANGELAND AGRICULTURE IN THE NORTHERN GREAT PLAINS

Project: 5434-11210-003-00D

Location: Miles City, Montana

Researchers: M. Haferkamp
E. Grings
R. Heitschmidt
R. Bellows
R. Short
M. MacNeil
M. Grosz

Objectives:

(1) For the mixed grass prairie in the Northern Great Plains quantify role of rangelands & management in regulating atmospheric carbon dioxide flux; identify ecological mechanisms and quantify impact of livestock grazing on long-term sustainability; quantify role of planted forages on ecological & economic sustainability of beef cattle industry; & elucidate interaction effects of soil water & nitrogen on herbage production & plant species composition between indigenous perennial & alien annual grass species.

Approach:

Field-laboratory studies will evaluate how plants respond to grazing and environmental stress. Role of rangelands and management tactics in regulating atmospheric carbon dioxide flux will be assessed by measuring temporal changes in plant biomass, soil organic matter and water, and carbon dioxide fluxes with both a Bowen-Ratio Unit and 1m**3 chambers. Long-term impacts of environment on ecological condition will be assessed by evaluating changes in plant species composition inside and outside livestock exclosures and evaluating changes in herbage production and rooting dynamics with short-term droughts applied with a rain-out shelter. The potential role of planted forages will be studied by monitoring herbage growth dynamics, cattle diets, & weight gains. Plant and community responses to interactions of varying levels of soil water and nitrogen will be assessed in field and greenhouse studies by measuring plant water relations, phenological development, and above- and below-ground biomass production at selected time intervals.

DEVELOP PHENOTYPIC/GENOTYPIC & NUTRIENT MANAGEMENT STRATEGIES FOR OPTIMIZING BEEF CATTLE PROD. IN NGP

Project: 5434-31000-008-00D

Location: Miles City, Montana

Researchers: E. Grings
R. Heitschmidt
R. Short
M. Haferkamp
R. Bellows
M. MacNeil
M. Grosz

Objectives:

(1) Quantify both plant and animal factors causing nutrient limitations to beef cattle production from rangeland in the Northern Great Plains and devise economically and environmentally sound management practices to overcome those limitations.

(2) Ascertain role of hypermuscularity gene(s) in rangeland beef cattle production by determining the effect that this trait has on body composition, quantity and quality of meat produced, nutrient requirements, grazing behavior, growth and reproduction.

Approach:

Cows will be bred to Piedmontese, Limosin & Hereford bulls to produce F1 progeny. F1 progeny will be inter se mated to produce F2 progeny. Progeny will be evaluated for nutritional requirements, reproductive traits, and carcass characteristics. Gene expression will be determined from analysis of distribution of phenotypic data based on muscle scores, ultrasound evaluation & histological & biochemical analysis of muscle samples. Blood and tissue samples will be collected for blood typing and DNA/protein analysis. Cows will be bred to calve during 3 calving periods from late winter to early summer. Nutritional tactics will be developed & tested for overcoming nutritional limitations imposed by these calving management strategies. Herbage, diet, & environmental characteristics will be monitored to evaluate the nutritional regimen under which the systems function and the interaction of the grazing animal with available rangeland resources. Digestion studies will be conducted to aid in understanding of the animal's response to nutrient supplementation strategies.

STRATEGIC FEEDING TO OPTIMIZE USE OF FEED RESOURCES BY DIVERSE BREEDS OF CATTLE AND SHEEP

Project: 5438-31000-035-00D

Location: Clay Center, Nebraska

Researchers: C. Ferrell
H. Freetly

Objectives:

(1) Develop strategies to decrease heifer development costs and increase their subsequent productivity.

(2) Develop strategies to optimize cow and ewe performance with reduced energy and protein supplementation.

Approach:

Dietary treatments will be imposed on prepubertal heifers of diverse breeds to elicit divergent patterns of growth. Response variables include age at conception, conception rate, calving difficulty, calf birth weight, calf growth patterns, weaning rate and weight. Alternative feeding strategies will be used on mature cows and ewes of divergent breeds to produce different patterns of body weight changes during the production year. Efficiency of energy and protein use will be assessed by feeding trials, nutrient balance studies and indirect calorimetry. Influence of dietary regimens on calf birth weight, postpartum interval of anestrus, conception rate and calf preweaning growth rate will be assessed. Alternative approaches to protein and energy supplementation will be evaluated by feeding and digestion trials. Nutrient absorption and intermediary metabolism will be determined by measuring net exchange of nutrients across tissues.

NUTRIENT CONSERVATION AND ODOR REDUCTION IN SWINE AND CATTLE CONFINEMENT FACILITIES

Project: 5438-31000-036-00D

Location: Clay Center, Nebraska

Researchers: V. Varel
D. Miller

Objectives:

Reduce nutrient loss and odor emissions from swine and cattle confinement facilities by 1) inhibiting microbial activities which produce offensive gaseous and volatile organic compounds, and 2) developing microbially enriched biofilters and biocovers which efficiently metabolize offensive odors to non-odorous compounds.

Approach:

Odor from livestock confinement is produced primarily from anaerobic microbial fermentation of the substrates in waste. Efficient, cost-effective solutions for odor management should include strategies that reduce initial odor production and treatment systems that optimize microbial conversion of odorous compounds to non-odorous compounds before being released. A variety of environmentally friendly compounds including bacteriostatic, bacteriocidal, and other microbial inhibitors will be evaluated for their ability to control odor production, limit greenhouse gas emissions, and reduce nutrient loss from livestock manures. Remaining offensive compounds will then be metabolized in microbially-enriched treatment systems. Microbial enrichments from agricultural soils will be selected for high efficiency odor-consumption and characterized using culture-based and molecular techniques. The most efficient bacteria will be seeded into air biofilters, waste biocovers, and feedlot soils for maximum removal of odorous compounds.

NUTRITIONAL AND MANAGEMENT STRATEGIES TO IMPROVE REPRODUCTIVE PERFORMANCE IN GILTS AND SOWS

Project: 5438-31000-040-00D

Location: Clay Center, Nebraska

Researchers: J. Klindt
J. Yen

Objectives:

Develop nutrition and management strategies to ensure:

(1) Gilts express puberty and conceive in a concise and timely manner.

(2) Sows mate and conceive within a timely interval after weaning.

Approach:

Nutritional environment, has short- and long-term effects on physiological development. A series of studies will be conducted to test the following hypotheses concerning the role of nutritional environment in determining reproductivity of gilts and sows: 1) Faster growing females cycle and conceive more readily than those gaining slower. 2) Dynamic measures of gain in females are more indicative of reproductivity than static measures of composition. 3) Faster gaining animals have patterns of hormone secretion and clearance different than slower gaining animals. 4) Faster gaining animals have higher rates of metabolism than those gaining slower. 5) Limit-fed developing animals acquire greater ability to mobilize and replenish tissue stores. 6) Inadequate bioavailability of metal-amino acid complexes to hypothalamus limit reproductivity of sows. Studies will use differing levels of nutrition, serial slaughter, calorimetry, measures of hormone and metabolite levels and clearance to identify effects of nutritional environment on reproductive efficiency.

METABOLISM AND NUTRITIONAL MANAGEMENT OF PROLIFIC SOWS DURING GESTATION AND LACTATION

Project: 5438-31000-050-00D

Location: Clay Center, Nebraska

Researchers: J. Pekas

Objectives:

(1) Develop feed management guidelines to improve nutrition during late gestation, lactation, and weaning/rebreeding of sows.

(2) Demonstrate physiological associations between the capacities for protein digestion versus protein ingestion.

Approach:

Studies will focus on dynamics and limits of reciprocal responses between protein intake and protein utilization. Effects of pattern and quantity of protein ingestion on turnover and secretion of endogenous digestive proteins, on protein digestibility, protein retention, and performance of the sow and progeny will be evaluated. Various strategies for acceleration or deceleration of dietary protein intake will be evaluated. Feed allowances adjusted upward to mimic exponential fetal growth during gestation, held at a high level during lactation, and adjusted downward after weaning will be compared to conventional feed management. Response criteria will include: number, birth weight, and weaning weight of piglets, loss of fat and weight from sows during lactation, return-to-estrus interval, 56-day litter gain, rate and efficiency of protein accretion by the progeny. Feeding strategies will be guided by growth and protein deposition of the gravid uterus, of milk protein secreted, and output of gastrointestinal endogenous proteins.

DEVELOPMENT OF AN EFFICIENT SYSTEM FOR PRODUCTION OF MEAT-TYPE PIGS IN THE SOUTHERN UNITED STATES

Project: 5438-31000-042-00D

Location: Clay Center, Nebraska

Researchers: R. Christenson

Objectives:

(1) Evaluate four (4) breeding lines for prolificacy and carcass characteristics.

(2) Develop feeding systems to obtain efficient biological conversion and minimize feed cost by using local feeds such as rice by-products as appropriate.

Approach:

Initially, a physical facility will be developed and an effective breeding and production program will be implemented to provide a basis for conducting swine production research. Lines of swine will be selected to establish maternal and paternal lines that can perform under the environmental conditions in the southern United States. A production program will be developed to ensure appropriate levels of fertility and litter size. Nutritional diets for swine at all stages of the life cycle that lead to optimum feed efficiency and rate of growth at lowest cost, utilizing local feeds whenever possible, will be established.

MANAGEMENT OF NUTRIENTS IMPACTING THE ENVIRONMENT FROM BEEF FEEDLOTS

Project: 5438-63000-008-00D

Location: Clay Center, Nebraska

Researchers: J. Nienaber
R. Eigenberg
B. Woodbury

Objectives:

(1) Refine nutrient fate linkages between feeding practices and manure collection, treatment, and utilization.

(2) Develop risk assessment tools for best management practices for manure treatment and utilization.

(3) Use linkages and risk assessment to refine waste management decision-making models.

Approach:

Linkages between nutrients fed, excreted, and available to crops will be investigated in MARC cattle feeding facilities, on cropland, and in the environmental laboratory. Management practices affecting nutrient availability include collection, treatment, storage and land application. Mass balance techniques will be used to evaluate volatilization losses while mapping of nutrient indicators will be used to assess risks because of excessive application. Decision-making tools include sensors to evaluate risks and models to guide rates of application so that environmentally acceptable conditions can be maintained within the system.

GENETIC CHANGE IN CALVING EASE AND QUANTITATIVE TRAIT LOCI DETECTION IN CATTLE POPULATIONS

Project: 5438-31000-048-00D

Location: Clay Center, Nebraska

Researchers: J. Nienaber
R. Eigenberg
B. Woodbury

Objectives:

(1) Estimate genetic change in calving ease of two-year-old heifers resulting from seven years of selection.

(2) Evaluate genetic changes in correlated traits to identify useful indicator traits and possible problems with this method of selection.

(3) Identify quantitative trait loci (QTL) for important meat, ovulation, and production traits in beef cattle.

(4) Develop methods to find QTL in existing cattle populations.

(5) Use selection herds to validate QTL effects and evaluate their potential use in beef cattle improvement.

Approach:

Substantial change in calving ease has been made during five years of selection in seven populations of cattle. Complete the final two years of selection for calving ease using multiple-trait genetic prediction methods. Use statistical methods to estimate genetic changes in heifer calving ease, birth weight, weaning weight, yearling weight, gestation length, pelvic area, and calf survival based on data collected while cattle were being selected. Slaughter a sample of steers from select and control lines to evaluate the effects of selection on carcass measurements. Use and develop quantitative methods to identify loci affecting traits within populations. Use a dense genetic marker map to identify quantitative loci in populations of cattle with differences in ovulation rate, muscularity, and meat quality. Structure and plan other populations to validate identified quantitative trait loci. This approach should identify methods that can be used for genetic improvement of livestock.

STRATEGIES TO OPTIMIZE CARCASS YIELD AND MEAT QUALITY OF RED MEAT ANIMALS

Project: 5438-31430-001-00D

Location: Clay Center, Nebraska

Researchers: M. Koohmaraie
S. Shackelford
T. Wheeler

Objectives:

1) Identify and validate genetic markers for carcass composition and meat tenderness.

(2) Develop an instrument procedure to accurately measure tenderness and red meat yield for beef.

(3) Obtain the necessary information to manipulate the systems regulating muscle growth and meat tenderness.

(4) Develop genetic and postmortem strategies to improve red meat yield and palatability.

(5) Evaluate effects of breeds representing diverse biological types on carcass composition and meat quality.

Approach:

Whole-genome linkage analysis will be used to identify genetic markers for carcass composition and meat tenderness. Will use knowledge of biological factors regulating meat tenderness to develop a tenderness-based beef classification system and strategies to improve meat tenderness. Detailed carcass composition and meat quality measurements will be used to evaluate breeds representing diverse biological types. Will utilize mRNA differential display, gene expression fingerprinting, and representational difference analysis of cDNA or other emerging methodologies to identify and characterize genes differentially expressed in callipyge lambs. Will determine the role of the calpain proteolytic system in muscle protein turnover by overexpression of bovine calpastatin cDNA in muscle cell lines and transgenic mice. By identifying and sequencing the calpastatin gene promoter, we will determine how expression of the calpastatin gene is regulated. Some of these experiments will be conducted in biosafety level 2 laboratories.

DYNAMIC SIMULATION MODEL FOR EVALUATION OF STRATEGIC BEEF CATTLE MANAGEMENT DECISIONS

Project: 5438-31630-001-00D

Location: Clay Center, Nebraska

Researchers: T. Jenkins
C. Williams

Objectives:

Develop software aids to provide decision support for managers in the beef cattle industry. These applications will incorporate dynamic model components of beef production with user friendly graphical interfaces. Specific components to be evaluated are reproduction, voluntary feed intake, animal waste emission, forage growth, and the forage-animal interface. Information characterizing the biological effects of management decision will serve as input for economic decisions.

Approach:

The reproductive component of an existing herd model and other existing reproductive models will be evaluated for biological accuracy using information for the MARC data bases. Voluntary feed intake data from both growing cattle and sheep will be analyzed to investigate variation in voluntary feed intake. Studies will be conducted to determine the effect of feed restriction on excretion of excess nutrients by cattle. Forage growth models will be identified with a model identified for coupling with a beef production model. User friendly graphical interfaces will be analyzed. A wastage model will be linked to a postweaning growth model allowing producers to monitor the environmental impact of waste management decisions. The total package will provide beef cattle producers with decision support aids aggregating information from research disciplines involved in animal agriculture production. Knowledge derived from this integration enhances the opportunity for producers to improve production efficiency.

IMPROVING FORAGE UTILIZATION BY STOCKERS IN SUSTAINABLE FORAGE LIVESTOCK SYSTEMS

Project: 6218-31630-003-00D

Location: El Reno, Oklahoma

Researchers: W. Phillips
M. Brown
J. Daniel
H. Mayeux, Jr.

Objectives:

(1) To determine and mitigate factors influencing forage intake and forage digestibility by stockers that limit growth and development.

(2) To identify and resolve factors that influence how stockers absorb and utilize energy and protein derived from forages.

(3) Develop management systems that optimize stocker growth and development but minimizes economic and environmental risk.

Approach:

The effect of forage species, combinations of grasses and legumes, previous stocker management, stocker genotype, stocker behavior and diet supplementation on rumen dynamics will be determined. Microbial population shifts and functionality, fermentation efficiency, rumen digestion rate and extent will be determined. Different genotypes of stockers will be used to determine the interaction between altering post-rumen nutrient output, animal genetics, and animal behavior on efficiency of energy and protein utilization. Production scale stocker systems developed through the integration of new plant and animal genetic material and innovative management will be tested to validate animal output, input requirements and the impact of the system on water and soil resource management.

INTEGRATED FARMING SYSTEMS FOR MID-SOUTH REGION

Project: 6227-12630-001-00D

Location: Booneville, Arkansas

Researchers: D. Pote
D. Brauner

Objectives:

To develop integrated farm systems that produce forages, livestock and tree-based products that are appropriate for small farmers and determine the environmental impact of such farming practices.

Approach:

Information from component research will be integrated into farming systems and the production efficiency and environmental impact of such systems will be tested. A forage system for lambing and lamb finishing will be compared to one combining lamb production with pine needle harvests. Botanical composition and forage yield of a common bermuda-tall fescue-arrowleaf clover mixture planted to pine trees will be compared to a mixture without trees for three years after tree planting. Later, these fields will be used to compare cow-calf production with and without pines. Studies will be conducted in 15-year old pine stands to assess soil and nutrient run-off as a function of various treatments to remove needles and supply nutrients. Effects of partial incorporation of poultry litter into a sod on forage production, and soil and nutrient run-off will be compared to surface application. The ability of selected tree species on stream and pond bank stabilization will be evaluated to determine mixtures of trees that maximize environmental protection with economic returns.

SUSTAINABLE LIVESTOCK-FORAGE SYSTEMS FOR SMALL FARMS IN THE MID-SOUTH

Project: 6227-21310-006-00D

Location: Booneville, Arkansas

Researchers: J. Burke
G. Aiken
D. Burner
D. Brauer

Objectives:

To improve the efficiency and sustainability of traditional forage-ruminant productions systems and develop production systems leading to alternative livestock products for small farms in the mid-south.

Approach:

Research will be aimed at cow-calf production, cattle stocker operations and the production of alternative ruminant meat products. Replicated field and grazing trials will be conducted on a variety of warm and cool season forages alone and in combinations to evaluate their agronomic potential in the mid-south region and doeage stand persistance/sustainability. Research on the establishment and maintenance of legumes in bermudagrass and tall fescue stands will be one area of focus in this research arena. Hormone levels and hormonal responses of tissues in cows and ewes grazing endophyte-free and -infected tall fescue will be compared to determine the effects of ergoalkaloids on reproductive responses. Results from such experiments will lead to the development of management practices that increases calving percentage of ruminants on tall fescue. Research will be initiated with sheep and lambs to determine best management practices to produce high quality market lambs with emphasis on reproductive performance, and forage-based finishing.

COMPREHENSIVE NUTRIENT MANAGEMENT TO IMPROVE POULTRY PRODUCTION

Project: 6406-63000-002-00D

Location: Mississippi State, Mississippi

Researchers: B. Lott
J. May
J. Simmons

Objectives:

(1) Develop nutrition and flock management procedures to reduce the amount of phosphorous in litter.

(2) Develop more efficient methods of handling and utilizing poultry litter to reduce nutrient losses to water and air.

Approach:

Experiments will determine the minimum dietary phosphorus levels required for environment, sex, and weight of birds. Broilers will be grown in temperatures common to commercial poultry, and diets will incorporate dietary phosphorus levels, phytase, and low phosphorus corn treatments. The amount of phosphorus in waste will be measured. Experiments will identify the nutrient specifications and treatments that minimize excreted phosphorus and maintain acceptable productivity under different environmental conditions. Experiments will improve the economics of transport and use of broiler litter for fertilizer. Procedures will include lengthening the period that litter is used, microbial and chemical treatments to sequester the excreted nitrogen, and mechanical separation to recycle components of litter. Bacteria that incorporate nitrogen from excreta into stable compounds will be identified. Cultures and conditions will be developed to enable sequestration of nitrogen without repeated chemical treatments.

UTILIZATION AND MANAGEMENT OF TROPICAL FORAGES FOR BEEF HEIFER AND BULL DEVELOPMENT IN THE SUBTROPCIAL US

Project: 6619-21630-003-00D

Location: Brooksville, Florida

Researchers: M. Williams
S. Coleman

Objectives:

(1) Evaluate forage-based systems for the development of replacement heifers and herd bulls under subtropical conditions.

(2) Develop environmentally sensitive and economically sound management strategies for warm-season forages with emphasis on longterm pasture stability, productivity, and nutritional quality.

Approach:

A series of short term plot/nutrition studies and multiyear grazing research projects will look at the effect and interaction of differing management options, including forage species, fertility, grazing system, and cattle breed, on animal nutrition and reproduction, forage productivity and persistence, environmental impact, and economic return. Plant response variables will include individual and whole stand establishment, stand persistence and productivity, and nutritive value. Animal responses evaluated will include grazing behavior (time, duration, and selectivity), reproductive performance (age at puberty, pregnancy rate and calving percent, and calving interval), metabolic response (blood urea nitrogen, rumen pH, and VFA's). Environmental aspects evaluated will include soil compaction, organic matter, rainfall infiltration rate, and weed encroachment.

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